

SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yuzhakov, Alexander
Yurieva, Olga
Jeruzalmi, David
Bruck, Irina
Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

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<211> 2007

<212> DNA

<213> *Thermus thermophilus*

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<212> PRT

<213> *Thermus thermophilus*

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Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
          35                      40                     45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
          50                      55                     60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
          65                      70                     75                     80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
          85                      90                     95

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Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu	100	105	110
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Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro	130	135	140
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro	145	150	155
Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu	165	170	175
Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg	180	185	190
Glu	Ala	Glu	Glu	Glu	Ala	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ala	Asp	Gly	195	200	205
Ala	Leu	Arg	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Arg	Phe	Leu	Leu	Leu	Glu	210	215	220
Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro	225	230	235
Gly	Thr	Gly	Val	Ala	Glu	Ile	Ala	Ala	Ser	Leu	Ala	Arg	Gly	Lys	Thr	245	250	255
Ala	Glu	Ala	Leu	Gly	Leu	Ala	Arg	Arg	Leu	Tyr	Gly	Glu	Gly	Tyr	Ala	260	265	270
Pro	Arg	Ser	Leu	Val	Ser	Gly	Leu	Leu	Glu	Val	Phe	Arg	Glu	Gly	Leu	275	280	285
Tyr	Ala	Ala	Phe	Gly	Leu	Ala	Gly	Thr	Pro	Leu	Pro	Ala	Pro	Pro	Gln	290	295	300
Ala	Leu	Ile	Ala	Ala	Met	Thr	Ala	Leu	Asp	Glu	Ala	Met	Glu	Arg	Leu	305	310	315
Ala	Arg	Arg	Ser	Asp	Ala	Leu	Ser	Leu	Glu	Val	Ala	Leu	Leu	Glu	Ala	325	330	335
Gly	Arg	Ala	Leu	Ala	Ala	Glu	Ala	Leu	Pro	Gln	Pro	Thr	Gly	Ala	Pro	340	345	350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
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 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
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 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
 450 455 460
 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
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 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
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<212> DNA

<213> *Thermus thermophilus*

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<210> 4

<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

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Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
      20              25              30

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Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
      35              40              45

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Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
      50              55              60

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Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
      65              70              75              80

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Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
      85              90              95

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Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro		
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225					230					235					240		
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Tyr	Ala	Ala	Phe	Gly	Leu	Ala	Gly	Thr	Pro	Leu	Pro	Ala	Pro	Pro	Gln		
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Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
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 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
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 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
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<210> 5
 <211> 454
 <212> PRT
 <213> Thermus thermophilus

<400> 5
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 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

85										90					95				
Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu				
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Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser				
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Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro				
	130					135					140								
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro				
145					150					155					160				
Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu				
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Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg				
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Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro				
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Ala	Glu	Ala	Leu	Gly	Leu	Ala	Arg	Arg	Leu	Tyr	Gly	Glu	Gly	Tyr	Ala				
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Pro	Arg	Ser	Leu	Val	Ser	Gly	Leu	Leu	Glu	Val	Phe	Arg	Glu	Gly	Leu				
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Ala	Arg	Arg	Ser	Asp	Ala	Leu	Ser	Leu	Glu	Val	Ala	Leu	Leu	Glu	Ala				
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Gly	Arg	Ala	Leu	Ala	Ala	Glu	Ala	Leu	Pro	Gln	Pro	Thr	Gly	Ala	Pro				

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Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro				
355		360		365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe				
370		375		380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg				
385		390		395
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Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys				
	405		410	415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro				
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Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu				
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Gly Glu Lys Lys Lys Ala				
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<210> 6
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
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32

<210> 7
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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cgcggaattcg tgctcsggsg gctcctcsag sgtc

34

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 9
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1 5

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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38

<210> 11
<211> 38
<212> DNA
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<210> 12
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<212> DNA
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<210> 14
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<210> 15
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<220>
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<210> 17
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<213> Artificial Sequence

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<223> X is any aa at position 2

<220>
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<400> 17
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1 5

<210> 18
<211> 12
<212> PRT
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<220>

<223> Description of Artificial Sequence: peptide

<400> 18

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

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Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
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Ala Leu Asp Val
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<210> 20
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 <212> PRT
 <213> Bacillus subtilis

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 Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
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 Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
 65 70 75 80
 Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
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 Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
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 Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
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 His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
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 Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
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 Arg Ile Thr Ser
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<210> 21
 <211> 294
 <212> PRT

<213> Escherichia coli

<400> 21

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Ser	Leu	Gly	Arg	Ile	His	His	Ala	Tyr	Leu	Phe	Ser	Gly	Thr	Arg	Gly	
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Val	Gly	Lys	Thr	Ser	Ile	Ala	Arg	Leu	Leu	Ala	Lys	Gly	Leu	Asn	Cys	
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Glu	Ile	Glu	Gln	Gly	Arg	Phe	Val	Asp	Leu	Ile	Glu	Ile	Asp	Ala	Ala	
			85					90						95		
Ser	Arg	Thr	Lys	Val	Glu	Asp	Thr	Arg	Asp	Leu	Leu	Asp	Asn	Val	Gln	
			100					105					110			
Tyr	Ala	Pro	Ala	Arg	Gly	Arg	Phe	Lys	Val	Tyr	Leu	Ile	Asp	Glu	Val	
		115					120					125				
His	Met	Leu	Ser	Arg	His	Ser	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	
	130					135						140				
Glu	Pro	Pro	Glu	His	Val	Lys	Phe	Leu	Leu	Ala	Thr	Thr	Asp	Pro	Gln	
145					150					155					160	
Lys	Leu	Pro	Val	Thr	Ile	Leu	Ser	Arg	Cys	Leu	Gln	Phe	His	Leu	Lys	
			165						170					175		
Ala	Leu	Asp	Val	Glu	Gln	Ile	Arg	His	Gln	Leu	Glu	His	Ile	Leu	Asn	
			180					185					190			
Glu	Glu	His	Ile	Ala	His	Glu	Pro	Arg	Ala	Leu	Gln	Leu	Leu	Ala	Arg	
		195					200					205				
Ala	Ala	Glu	Gly	Ser	Leu	Arg	Asp	Ala	Leu	Ser	Leu	Thr	Asp	Gln	Ala	
	210					215					220					
Ile	Ala	Ser	Gly	Asp	Gly	Gln	Val	Ser	Thr	Gln	Ala	Val	Ser	Ala	Met	
225					230					235					240	

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285

Leu His Arg Ile Ala Met
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
 165 170 175
 Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
 180 185 190
 Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
 195 200 205
 Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
 210 215 220
 Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
 225 230 235 240
 Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
 245 250 255
 His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
 260 265 270
 Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
 275 280 285
 Leu His Gln Ile Ala Leu
 290

<210> 23
 <211> 294
 <212> PRT
 <213> Bacillus subtilis

<400> 23
 Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
 1 5 10 15
 Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
 20 25 30
 Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
 35 40 45
 Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
 50 55 60
 Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65		70		75		80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala						
	85		90		95	
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys						
	100		105		110	
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val						
	115		120		125	
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu						
	130		135		140	
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His						
	145		150		155	160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys						
	165		170		175	
Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp						
	180		185		190	
Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser						
	195		200		205	
Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala						
	210		215		220	
Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile						
	225		230		235	240
Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu						
	245		250		255	
His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu						
	260		265		270	
Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr						
	275		280		285	
Phe Arg Asp Met Leu Leu						
	290					

<210> 24

<211> 300

<212> PRT

<213> Caulobacter crescentus

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
 245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
 260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
 275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
 290 295 300

<210> 25
 <211> 260
 <212> PRT
 <213> Mycoplasma genitalium

<400> 25
 Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
 1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
 20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
 35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
 50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
 65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
 85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
 100 105 110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
 115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
 130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
 145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
 165 170 175
 Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
 180 185 190
 Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
 195 200 205
 Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
 210 215 220
 Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
 225 230 235 240
 Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
 245 250 255
 Tyr Gln Glu Ile
 260

<210> 26
 <211> 289
 <212> PRT
 <213> Thermus thermophilus

<400> 26
 Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100					105					110						
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser	
115					120					125						
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro	
130					135					140						
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro	
145					150					155					160	
Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu	
165					170					175						
Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg	
180					185					190						
Glu	Ala	Glu	Glu	Glu	Ala	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ala	Asp	Gly	
195					200					205						
Ala	Leu	Arg	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Arg	Phe	Leu	Leu	Leu	Glu	
210					215					220						
Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro	
225					230					235					240	
Gly	Thr	Gly	Val	Ala	Glu	Ile	Ala	Ala	Ser	Leu	Ala	Arg	Gly	Lys	Thr	
245					250					255						
Ala	Glu	Ala	Leu	Gly	Leu	Ala	Arg	Arg	Leu	Tyr	Gly	Glu	Gly	Tyr	Ala	
260					265					270						
Pro	Arg	Ser	Leu	Val	Ser	Gly	Leu	Leu	Glu	Val	Phe	Arg	Glu	Gly	Leu	
275					280					285						

Tyr

<210> 27

<211> 94

<212> DNA

<213> Thermus thermophilus

<400> 27

gccggaggga gaaaaaaaaa gccgagccca aggccccgcc cggccccacc ccgaagcgcc 60
cgcacccccg ggccccccga ggaggaggag aggc 94

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac 23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

<220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc 25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggscststcs gagcagaag 29

<210> 33
<211> 34

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 33
 gcgggacacct caacgaggac ctctccatct tcaa 34

 <210> 34
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 34
 gcgggacacct tgcgtcsag sgtsagsgcg tcgta 35

 <210> 35
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 35
 gggaaggacc agcgcgctact cccctgctc ctaggtgtg 39

 <210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 36
 gtgtggatcc ttcttcttsc ccatsgc 27

 <210> 37
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 37
 caccgattcc agtggtgcct aggtgtg 27

 <210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 38
 caacacctgg tgttccagga gcctgtgctt 30

 <210> 39
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 39
 ccagaatcgt ctgctgggtcg tag 23

 <210> 40
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 40
 agcaccctgg aggagcttc 19

 <210> 41
 <211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsgtsnns acnns gagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctcggtg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccttgcg gctccgggtg

30

<210> 46
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 46
 gcgctctaga cgagttccca aagcgtgcgg t 31

 <210> 47
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 47
 cgcgctctaga tcacctgtat ccaga 25

 <210> 48
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 48
 gcggcgcata tgggtggtggt cctggacctg gag 33

 <210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 49
 cgcgctctaga tcacctgtat ccaga 25

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 50
gtsctsgtsa agacscactt 20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 51
sagsagsgcg ttgaasgtgt g 21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 52
ctcgttggtg aaagtttccg tg 22

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 53
ctcgttggtg aaagtttccg tg 22

<210> 54
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 54
 tctggcaaca cgttctggag cacatcc 27

 <210> 55
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 55
 tgctggcggt catcttcagg atg 23

 <210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 56
 catcctgaag atgaacgcca gca 23

 <210> 57
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 57
 aggttatcca caggggtcat gtgca 25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac ggttcccaa 29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

<210> 62
<211> 8

<212> PRT
 <213> Thermus thermophilus

 <400> 62
 Phe Phe Ile Glu Ile Gln Asn His
 1 5

 <210> 63
 <211> 8
 <212> PRT
 <213> Thermus thermophilus

 <400> 63
 Tyr Asp Ala Leu Thr Leu Asp Asp
 1 5

 <210> 64
 <211> 6
 <212> PRT
 <213> Thermus thermophilus

 <400> 64
 Ala Met Gly Lys Lys Lys
 1 5

 <210> 65
 <211> 9
 <212> PRT
 <213> Thermus thermophilus

 <400> 65
 Phe Asn Lys Ser His Ser Ala Ala Tyr
 1 5

 <210> 66
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: peptide

 <220>
 <221> PEPTIDE

<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 68
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 69
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 69
Val Leu Val Lys Thr His Leu
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 70
His Arg Ala Leu Tyr Asp
1 5

<210> 71
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 71
His Thr Phe Asn Ala Leu Leu
1 5

<210> 72
<211> 34
<212> PRT
<213> Escherichia coli

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> *Rickettsia prowazekii*

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> *Helicobacter pylori*

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> *Synechocystis* sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78

<211> 34

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82

<211> 46

<212> PRT

<213> Rickettsia prowazekii

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83

<211> 45

<212> PRT

<213> Helicobacter pylori

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84

<211> 46

<212> PRT

<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

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gccttggcca tgaccgacca cggcaacctc ttcggggccg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240
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gccctctcgg ggtgcctcgg ggcggagatc ccccagttca tctccagga ccgtctggac 480
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cgaaagtacg gcctggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660
gcccgcgccc acgaggtcct cctcgccatc cagtccaaga gcaccctgga cgaccccggg 720
cgctggcgct tcccctgcga cgagttctac gtgaagaccc ccgaggagat gcgggccatg 780
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cccgaggggc	ggaccgaggc	ccagtacctc	atggagctca	ccttcaaggg	gctcctccgc	960
cgctaccccg	accggatcac	cgagggtctc	taccgggagg	tcttccgcct	tttggggaag	1020
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gtggccatgc	gcctggaggg	cctgaaccgc	cacgcctccg	tccacgccgc	cggggtggtg	1740
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gtcaccacgt	acgacatggg	ggcgggtggg	gccttggggc	ttttgaagat	ggactttttg	1860
ggcctccgca	ccctcacctt	cctggacgag	gtcaagcgca	togtcaaggc	gtcccagggg	1920
gtggagctgg	actacgatgc	cctccccctg	gacgacccca	agaccttcgc	cctcctctcc	1980
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cccatggagc	acatccccac	ctacatccgc	cgccaccacg	ggctggagcc	cgtgagctac	2160
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ggaggtcctt	ctccagggcg	gccaggcggg	ggaggcccag	gaggcggtgc	ccttctaggg	3660
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<210> 87

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His		
210	215	220
Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly		
225	230	235 240
Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu		
245	250	255
Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu		
260	265	270
Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly		
275	280	285
Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg		
290	295	300
Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg		
305	310	315 320
Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg		
325	330	335
Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu		
340	345	350
Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser		
355	360	365
Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe		
370	375	380
His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro		
385	390	395 400
Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys		
405	410	415
Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val		
420	425	430
Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu		
435	440	445
Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile		
450	455	460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val			
465	470	475	480
Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly			
	485	490	495
Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly			
	500	505	510
Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln			
	515	520	525
Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu			
	530	535	540
Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu			
545	550	555	560
Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala			
	565	570	575
Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu			
	580	585	590
Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala			
	595	600	605
Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr			
	610	615	620
Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly			
625	630	635	640
Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe			
	645	650	655
Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser			
	660	665	670
Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu			
	675	680	685
Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His			
	690	695	700
Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr			
705	710	715	720

Ser	Glu	Phe	Pro	His	Ala	Glu	Lys	Tyr	Leu	Lys	Pro	Ile	Leu	Asp	Glu	
				725					730					735		
Thr	Tyr	Gly	Ile	Pro	Val	Tyr	Gln	Glu	Gln	Ile	Met	Gln	Ile	Ala	Ser	
			740					745					750			
Ala	Val	Ala	Gly	Tyr	Ser	Leu	Gly	Glu	Ala	Asp	Leu	Leu	Arg	Arg	Ser	
		755					760					765				
Met	Gly	Lys	Lys	Lys	Val	Glu	Glu	Met	Lys	Ser	His	Arg	Glu	Arg	Phe	
	770					775					780					
Val	Gln	Gly	Ala	Lys	Glu	Arg	Gly	Val	Pro	Glu	Glu	Glu	Ala	Asn	Arg	
785					790				795					800		
Leu	Phe	Asp	Met	Leu	Glu	Ala	Phe	Ala	Asn	Tyr	Gly	Phe	Asn	Lys	Ser	
			805					810					815			
His	Ala	Ala	Ala	Tyr	Ser	Leu	Leu	Ser	Tyr	Gln	Thr	Ala	Tyr	Val	Lys	
			820					825					830			
Ala	His	Tyr	Pro	Val	Glu	Phe	Met	Ala	Ala	Leu	Leu	Ser	Val	Glu	Arg	
		835					840					845				
His	Asp	Ser	Asp	Lys	Val	Ala	Glu	Tyr	Ile	Arg	Asp	Ala	Arg	Ala	Met	
	850					855				860						
Gly	Ile	Glu	Val	Leu	Pro	Pro	Asp	Val	Asn	Arg	Ser	Gly	Phe	Asp	Phe	
865				870					875					880		
Leu	Val	Gln	Gly	Arg	Gln	Ile	Leu	Phe	Gly	Leu	Ser	Ala	Val	Lys	Asn	
			885					890					895			
Val	Gly	Glu	Ala	Ala	Ala	Glu	Ala	Ile	Leu	Arg	Glu	Arg	Glu	Arg	Gly	
			900					905					910			
Gly	Pro	Tyr	Arg	Ser	Leu	Gly	Asp	Phe	Leu	Lys	Arg	Leu	Asp	Glu	Lys	
		915					920				925					
Val	Leu	Asn	Lys	Arg	Thr	Leu	Glu	Ser	Leu	Ile	Lys	Ala	Gly	Ala	Leu	
	930					935					940					
Asp	Gly	Phe	Gly	Glu	Arg	Ala	Arg	Leu	Leu	Ala	Ser	Leu	Glu	Gly	Leu	
945				950						955					960	
Leu	Lys	Trp	Ala	Ala	Glu	Asn	Arg	Glu	Lys	Ala	Arg	Ser	Gly	Met	Met	
			965					970					975			

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
 980 985 990

Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
 995 1000 1005

Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
 1010 1015 1020

Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
 1025 1030 1035 1040

Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
 1045 1050 1055

Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
 1060 1065 1070

Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
 1075 1080 1085

Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
 1090 1095 1100

Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
 1105 1110 1115 1120

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
 1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
 1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
 1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
 1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
 1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
 1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
 1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88
<211> 198
<212> PRT
<213> Thermus thermophilus

<400> 88
Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15
Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30
Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45
Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
50 55 60
Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80
Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95
Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110
Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125
Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140
Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160
Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175
Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190
Tyr Met Leu Thr Ser Gly
195

<210> 89
 <211> 182
 <212> PRT
 . <213> Deinococcus radiodurans

 <220>
 <221> PEPTIDE
 <222> (79)
 <223> X at position 79 is undefined

<400> 89
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1 5 10 15

 Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
 20 25 30

 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
 35 40 45

 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
 50 55 60

 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
 65 70 75 80

 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
 85 90 95

 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
 100 105 110

 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
 115 120 125

 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
 130 135 140

 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
 145 150 155 160

 Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
 165 170 175

 Glu Leu Leu Gly Glu Arg
 180

<210> 90
 <211> 201
 <212> PRT
 <213> Bacillus subtilis

<400> 90

His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1 5 10 15

Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
 20 25 30

Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
 35 40 45

Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
 50 55 60

Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
 65 70 75 80

Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
 85 90 95

Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
 100 105 110

Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
 115 120 125

Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
 130 135 140

Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
 145 150 155 160

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 165 170 175

His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
 180 185 190

Lys Met Leu Lys Asp Ala Ala Glu Lys
 195 200

<210> 91
 <211> 188
 <212> PRT
 <213> Haemophilus influenzae

<220>
 <221> PEPTIDE
 <222> (47)
 <223> X at position 47 is undefined

<220>
 <221> PEPTIDE
 <222> (57)
 <223> X at position 57 is undefined

<400> 91
 Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
 1 5 10 15
 Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
 20 25 30
 Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
 35 40 45
 Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
 50 55 60
 His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
 65 70 75 80
 Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
 85 90 95
 His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
 100 105 110
 Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
 115 120 125
 Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
 130 135 140
 Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
 145 150 155 160
 Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
 165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92

<211> 189

<212> PRT

<213> Escherichia coli

<400> 92

Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80

Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95

His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
100 105 110

Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
115 120 125

Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140

Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145 150 155 160

His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175

Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
 <211> 201
 <212> PRT
 <213> Helicobacter pylori

<400> 93

Asn	Leu	Glu	Tyr	Leu	Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser
1				5					10					15	
Glu	Asn	Leu	Ile	Thr	Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu
			20					25					30		
Val	Phe	Ser	Phe	Ile	Asp	Leu	Glu	Thr	Thr	Gly	Ser	Cys	Pro	Ile	Lys
		35					40					45			
His	Glu	Ile	Leu	Glu	Ile	Gly	Ala	Val	Gln	Val	Lys	Gly	Gly	Glu	Ile
		50				55					60				
Ile	Asn	Arg	Phe	Glu	Thr	Leu	Val	Lys	Val	Lys	Ser	Val	Pro	Asp	Tyr
65						70				75					80
Ile	Ala	Glu	Leu	Thr	Gly	Ile	Thr	Tyr	Glu	Asp	Thr	Leu	Asn	Ala	Pro
				85					90					95	
Ser	Ala	His	Glu	Ala	Leu	Gln	Glu	Leu	Arg	Leu	Phe	Leu	Gly	Asn	Ser
			100					105					110		
Val	Phe	Val	Ala	His	Asn	Ala	Asn	Phe	Asp	Tyr	Asn	Phe	Leu	Gly	Arg
		115					120					125			
Tyr	Phe	Val	Glu	Lys	Leu	His	Cys	Pro	Leu	Leu	Asn	Leu	Lys	Leu	Cys
		130				135					140				
Thr	Leu	Asp	Leu	Ser	Lys	Arg	Ala	Ile	Leu	Ser	Met	Arg	Tyr	Ser	Leu
145					150					155					160
Ser	Phe	Leu	Lys	Glu	Leu	Leu	Gly	Phe	Gly	Ile	Glu	Val	Ser	His	Arg
			165						170					175	
Ala	Tyr	Ala	Asp	Ala	Leu	Ala	Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu
			180					185					190		
Leu	Asn	Leu	Pro	Ser	Tyr	Ile	Lys	Thr							
		195					200								

<210> 94
 <211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

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gggctttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gaggggggga ggcgcctccc cttccagagc ctcgctccggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catcccccg gaggccctgg aggaggcccc ctccctggag 300
gaggttctgg agaaggccta ccccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttcct ccgcccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccggtggtg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgccc tctccgaggt cctggagctt ccccgaagga cctgccaccg ggccctcgag 540
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ccccgcacgc tttgggaact cgggaggtag 630
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<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

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Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1             5             10            15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
    20             25            30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
    35             40            45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
    50             55            60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
    65             70            75            80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
    85             90            95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
    100            105            110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
    115            120            125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
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130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155 160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
	165	170 175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
	180	185 190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
	195	200 205
Arg Glx		
210		

<210> 96
 <211> 461
 <212> PRT
 <213> Pseudomonas marcesans

<400> 96
 Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn
 1 5 10 15
 Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser
 20 25 30
 Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser
 35 40 45
 Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala
 50 55 60
 Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala
 65 70 75 80
 Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro
 85 90 95
 Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu
 100 105 110
 Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe
 115 120 125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala		
130						135					140						
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile		
145					150					155					160		
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly		
				165					170					175			
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser		
			180					185					190				
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg		
	195						200					205					
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val		
	210					215					220						
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe		
225					230					235					240		
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu		
				245					250					255			
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu		
			260					265					270				
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp		
		275					280					285					
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg		
	290					295					300						
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr		
305					310					315					320		
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe		
				325					330					335			
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met		
			340					345					350				
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu		
	355						360					365					
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser		
	370					375					380						

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
 385 390 395 400
 Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
 405 410 415
 Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
 420 425 430
 Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
 435 440 445
 Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
 450 455 460
 <210> 97
 <211> 447
 <212> PRT
 <213> Synechocystis sp.
 <400> 97
 Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1 5 10 15
 Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
 20 25 30
 Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35 40 45
 Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50 55 60
 Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65 70 75 80
 Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
 85 90 95
 Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
 100 105 110
 Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115 120 125
 Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
 145 150 155 160
 Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val
 165 170 175
 Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
 180 185 190
 Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
 195 200 205
 Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
 210 215 220
 Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
 225 230 235 240
 Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
 245 250 255
 Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
 260 265 270
 Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
 275 280 285
 Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
 290 295 300
 Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala
 305 310 315 320
 Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
 325 330 335
 Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
 340 345 350
 Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
 355 360 365
 Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
 370 375 380
 Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
 385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

165	170	175
Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser		
180	185	190
Ile Arg Asp Asn Lys Ala Val Asp Phe Arg Asn Arg Tyr Arg Asn Val		
195	200	205
Asp Val Leu Leu Ile Asp Asp Ile Gln Phe Leu Ala Gly Lys Glu Gln		
210	215	220
Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser		
225	230	235
Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr		
245	250	255
Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp		
260	265	270
Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys		
275	280	285
Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile		
290	295	300
Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile		
305	310	315
Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp		
325	330	335
Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys		
340	345	350
Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn		
355	360	365
Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala		
370	375	380
Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser		
385	390	395
Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr		
405	410	415
Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu		

420

425

430

Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 440 445

<210> 99

<211> 507

<212> PRT

<213> Mycobacterium tuberculosis

<400> 99

Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15

Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30

Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45

Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60

Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80

Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95

Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110

Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125

Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140

His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160

Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175

Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
 180 185 190

Ile	Ala	Glu	Ala	Pro	Ala	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Trp	Gly	
	195						200					205				
Glu	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	Ala	Ala	Gly	Asn	Tyr	
	210					215					220					
Ala	Gln	Arg	Leu	Phe	Pro	Gly	Met	Arg	Val	Lys	Tyr	Val	Ser	Thr	Glu	
225					230					235					240	
Glu	Phe	Thr	Asn	Asp	Phe	Ile	Asn	Ser	Leu	Arg	Asp	Asp	Arg	Lys	Val	
			245						250					255		
Ala	Phe	Lys	Arg	Ser	Tyr	Arg	Asp	Val	Asp	Val	Leu	Leu	Val	Asp	Asp	
		260						265					270			
Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Gly	Ile	Gln	Glu	Glu	Phe	Phe	His	
	275						280					285				
Thr	Phe	Asn	Thr	Leu	His	Asn	Ala	Asn	Lys	Gln	Ile	Val	Ile	Ser	Ser	
	290					295					300					
Asp	Arg	Pro	Pro	Lys	Gln	Leu	Ala	Thr	Leu	Glu	Asp	Arg	Leu	Arg	Thr	
305					310					315					320	
Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp	Val	Gln	Pro	Pro	Glu	Leu	Glu	
				325					330					335		
Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys	Ala	Gln	Met	Glu	Arg	Leu	Ala	
		340						345					350			
Val	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ile	Ala	Ser	Ser	Ile	Glu	Arg	Asn	
		355					360					365				
Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Val	Thr	Ala	Phe	Ala	Ser	
	370					375					380					
Leu	Asn	Lys	Thr	Pro	Ile	Asp	Lys	Ala	Leu	Ala	Glu	Ile	Val	Leu	Arg	
385					390					395					400	
Asp	Leu	Ile	Ala	Asp	Ala	Asn	Thr	Met	Gln	Ile	Ser	Ala	Ala	Thr	Ile	
			405						410					415		
Met	Ala	Ala	Thr	Ala	Glu	Tyr	Phe	Asp	Thr	Thr	Val	Glu	Glu	Leu	Arg	
		420						425					430			
Gly	Pro	Gly	Lys	Thr	Arg	Ala	Leu	Ala	Gln	Ser	Arg	Gln	Ile	Ala	Met	
	435						440					445				

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
 450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
 465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
 485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
 500 505

<210> 100

<211> 446

<212> PRT

<213> Thermus thermophilus

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
 145 150 155 160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
165 170 175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
180 185 190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
195 200 205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
210 215 220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
225 230 235 240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
245 250 255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
260 265 270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
275 280 285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
290 295 300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
305 310 315 320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
325 330 335
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
340 345 350
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
355 360 365
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
370 375 380
Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg
385 390 395 400
Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
405 410 415

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101
<211> 467
<212> PRT
<213> Escherichia coli

<400> 101
Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

180	185	190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln		
195	200	205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg		
210	215	220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe		
225	230	235
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala		
245	250	255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro		
260	265	270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp		
275	280	285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala		
290	295	300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu		
305	310	315
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu		
325	330	335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg		
340	345	350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala		
355	360	365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala		
370	375	380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser		
385	390	395
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu		
405	410	415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg		
420	425	430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg		

435 440 445
 Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
 450 455 460

 Leu Ser Ser
 465

 <210> 102
 <211> 440
 <212> PRT
 <213> *Thermatoga maritima*

 <400> 102
 Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
 1 5 10 15

 Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
 20 25 30

 Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
 35 40 45

 Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
 50 55 60

 Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
 65 70 75 80

 Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
 85 90 95

 Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
 100 105 110

 Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
 115 120 125

 Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr
 130 135 140

 His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
 145 150 155 160

 Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
 165 170 175

Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg	180	185	190
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly	195	200	205
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His	210	215	220
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys	225	230	235
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu	245	250	255
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala	260	265	270
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu	275	280	285
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly	290	295	300
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val	305	310	315
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn	325	330	335
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala	340	345	350
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn	355	360	365
Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn	370	375	380
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser	385	390	395
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu	405	410	415
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu	420	425	430

Ile Ser Arg Arg Ala Leu Ser Gly
 435 440

<210> 103

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
 20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
 35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
 50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
 65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
 85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
 100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
 115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
 130 135 140

Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
 145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
 165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
 180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
 195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
 210 215 220

Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
 225 230 235 240

Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
 245 250 255

Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
 260 265 270

Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
 275 280 285

Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
 290 295 300

Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
 305 310 315 320

Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
 325 330 335

Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
 340 345 350

Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
 355 360 365

Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
 370 375 380

Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
 385 390 395 400

Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
 405 410 415

Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val
 420 425 430

Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp
 435 440 445

Lys Lys Thr Ala Phe Asn Ser Ser Glu
 450 455

<210> 104
 <211> 1305
 <212> DNA
 <213> *Thermus thermophilus*

<400> 104
 gtgtcgcacg aggccgtctg gcaacacggt ctggagcaca tccgccgcag catcaccgag 60
 gtggagtcc acacctggtt tgaaaggatc cgccccttgg ggatccggga cggggtgctg 120
 gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180
 atccaggagg gccctcggct cctcggggcc caggcgcccc ggtttgagct ccgggtggtg 240
 cccggggtcg tagtccagga ggacatcttc cagccccgc cgagcccccc ggcccaagct 300
 caaccggaag atacctttaa aacttcgtgg tggggcccaa caactccatg gcccacggc 360
 ggcgccgtgg ccgtggccga gtcccccggc cgggcctaca accccctctt catctacggg 420
 ggccgtggcc tgggaaagac ctacctgatg cagcccggtg gccactccg tgcgaagcgc 480
 ttccccca tggagattaga gtacgtttcc acggaactt tcaccaacga gctcatcaac 540
 cggccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600
 ctgctggtgg acgacgtcca gttcatcgcc ggaaaggagc gcaccagga ggagtttttc 660
 cacaccttca acgcccctta cgaggccac aagcagatca tcctctctc cgaccggccg 720
 cccaaggaca tcctcaccct ggaggcgcg ctcgggagcc gctttgagtg gggcctgatc 780
 accgacaatc cagccccga cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840
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 atccgggagt ggggaagggc cctcatgcgg gcacgcctt tcgcctccct caacggcggt 960
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 gcggaccctt tgagatcat ccgcaaagcg gcgggaccag ttcggcctga aaccgccgga 1080
 ggagctcacg gggagcgccg caagaaggag gtggtcctcc ccggcagct cgccatgtac 1140
 ctggtgcggg agctcaccct ggccctcctg cccgagatcg accagctcaa cgacgaccgg 1200
 gaccacacca cggctcctta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260
 gaggtgcagg gcctcctccg caccctccg gaggcgtgca catga 1305

<210> 105
 <211> 434
 <212> PRT
 <213> *Thermus thermophilus*

<400> 105
 Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15
 Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30
 Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45
 Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50	55	60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val		
65	70	75 80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro		
	85	90 95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly		
	100	105 110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser		
	115	120 125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu		
	130	135 140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg		
145	150	155 160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn		
	165	170 175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg		
	180	185 190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe		
	195	200 205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn		
	210	215 220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro		
225	230	235 240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu		
	245	250 255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile		
	260	265 270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp		
	275	280 285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp		
	290	295 300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val		

305		310		315		320
Glu Leu Thr Arg	Ala Val Ala Ala	Lys Ala Leu Arg	His Leu Arg	Pro		
	325		330		335	
Arg Glu Leu Glu	Ala Asp Pro Leu	Glu Ile Ile Arg	Lys Ala Ala	Gly		
	340		345		350	
Pro Val Arg Pro	Glu Thr Pro Gly	Gly Ala His Gly	Glu Arg Arg	Lys		
	355		360		365	
Lys Glu Val Val	Leu Pro Arg Gln	Leu Ala Met Tyr	Leu Val Arg	Glu		
	370		375		380	
Leu Thr Pro Ala	Ser Leu Pro Glu	Ile Asp Gln Leu	Asn Asp Asp	Arg		
385		390		395		400
Asp His Thr Thr	Val Leu Tyr Ala	Ile Gln Lys Val	Gln Glu Leu	Ala		
	405		410		415	
Glu Ser Asp Arg	Glu Val Gln Gly	Leu Leu Arg Thr	Leu Arg Glu	Ala		
	420		425		430	

Cys Thr

<210> 106

<211> 1128

<212> DNA

<213> *Thermus thermophilus*

<400> 106

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atgaacataa cggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcatac 60
gtccccctcta gaagcgccaa cccctcttac acctacctgg ggctttacgc cgaggaagg 120
gccttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180
gccccaaagcc ttccccgggt gctcgtcccc gccagccct tcttcagct ggtgcgagc 240
cttctgggg acctcgtggc cctcggcctc gcctcggagc cgggccaggg ggggcagctg 300
gagctctcct ccgggcgttt ccgcacccgg ctgagcctgg cccctgccga gggctacccc 360
gagcttcttg tgcccagggg ggaggacaag ggggccttcc ccctcggac gcgatgccc 420
tccggggagc tcgtcaaggc cttgaccac gtgcgctacg ccgcgagcaa cgaggagtac 480
cgggccatct tccgcggggg gcagctggag ttctcccccc agggcttcg ggcggtggcc 540
tccgacgggt accgcctcgc cctctacgac ctgcccctgc cccaagggtt ccaggccaag 600
gccgtggtcc ccgcccggag cgtggacgag atggtgcggg tcctgaaggg ggcggacggg 660
gccgagggcg tctcgcctt gggcgagggg gtgttgcccc tggccctcga gggcggaagc 720
gggggtccgga tggccctccg cctcatggaa ggggagttcc ccgactacca gaggtcatc 780
ccccaggagt tcgcctcaa ggtccagggt gagggggagg ccctcaggga ggcggtgcgc 840
cgggtgagcg tcctctccga ccggcagaac caccgggtgg acctcctttt ggaggaaggc 900

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cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgccag 960
 gtggaggggc cggacatggc cgtggcctac aacgcccgct acctcctcga ggccctcgcc 1020
 cccgtggggg accggggcca cctgggcatc tccggggcca cgagcccgag cctcatctgg 1080
 ggggacgggg aggggtaccg ggcggtggtg gtgccctca ggggtctag 1128

<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285
 Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300
 Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320
 Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335
 Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350
 Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365
 Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 108

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
355 360 365

Val Val Val Pro Leu Arg Val Glx
370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115		120		125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe				
130		135		140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe				
145		150		155
				160
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg				
		165		170
				175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser				
		180		185
				190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp				
		195		200
				205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg				
		210		215
				220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg				
225		230		235
				240
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu				
		245		250
				255
Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile				
		260		265
				270
Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn				
		275		280
				285
Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu				
		290		295
				300
Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn				
305		310		315
				320
Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val				
		325		330
				335
Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala				
		340		345
				350
Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx				
		355		360
				365

<210> 110
 <211> 367
 <212> PRT
 <213> *Proteus mirabilis*

<400> 110
 Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15
 Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30
 Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45
 Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
 50 55 60
 Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
 65 70 75 80
 Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
 85 90 95
 Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110
 Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
 115 120 125
 Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
 130 135 140
 Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
 145 150 155 160
 Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175
 Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
 180 185 190
 Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
 195 200 205
 Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
 210 215 220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
 245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
 260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
 275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
 290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
 305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
 325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
 340 345 350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
 355 360 365

<210> 111
 <211> 366
 <212> PRT
 <213> Haemophilus influenzae

<400> 111
 Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
 20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Ser Glu
 50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
 65 70 75 80

Thr	Leu	Ser	Asp	Asp	Ser	Glu	Ile	Thr	Val	Thr	Phe	Glu	Gln	Asp	Arg	85	90	95
Ala	Leu	Val	Gln	Ser	Gly	Arg	Ser	Arg	Phe	Thr	Leu	Ala	Thr	Gln	Pro	100	105	110
Ala	Glu	Glu	Tyr	Pro	Asn	Leu	Thr	Asp	Trp	Gln	Ser	Glu	Val	Asp	Phe	115	120	125
Glu	Leu	Pro	Gln	Asn	Thr	Leu	Arg	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe	130	135	140
Ser	Met	Ala	Asn	Gln	Asp	Ala	Arg	Tyr	Phe	Leu	Asn	Gly	Met	Lys	Phe	145	150	155
Glu	Thr	Glu	Gly	Asn	Leu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175
Leu	Ala	Val	Cys	Thr	Ile	Ser	Leu	Glu	Gln	Glu	Leu	Gln	Asn	His	Ser	180	185	190
Val	Ile	Leu	Pro	Arg	Lys	Gly	Val	Leu	Glu	Leu	Val	Arg	Leu	Leu	Glu	195	200	205
Thr	Asn	Asp	Glu	Pro	Ala	Arg	Leu	Gln	Ile	Gly	Thr	Asn	Asn	Leu	Arg	210	215	220
Val	His	Leu	Lys	Asn	Thr	Val	Phe	Thr	Ser	Lys	Leu	Ile	Asp	Gly	Arg	225	230	235
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Arg	Asn	Ala	Thr	Lys	Ile	Val	245	250	255
Glu	Gly	Asn	Trp	Glu	Met	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ser	Ile	260	265	270
Leu	Ser	Asn	Glu	Arg	Ala	Arg	Ser	Val	Arg	Leu	Ser	Leu	Lys	Glu	Asn	275	280	285
Gln	Leu	Lys	Ile	Thr	Ala	Ser	Asn	Thr	Glu	His	Glu	Glu	Ala	Glu	Glu	290	295	300
Ile	Val	Asp	Val	Asn	Tyr	Asn	Gly	Glu	Glu	Leu	Glu	Val	Gly	Phe	Asn	305	310	315
Val	Thr	Tyr	Ile	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Asn	Gln	Val	325	330	335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
355 360 365

<210> 112
<211> 367
<212> PRT
<213> Pseudomonas putida

<400> 112
Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

180	185	190
Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu		
195	200	205
Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile		
210	215	220
Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly		
225	230	235
Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu		
245	250	255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala		
260	265	270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala		
275	280	285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu		
290	295	300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe		
305	310	315
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln		
325	330	335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu		
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355	360	365

<210> 113
 <211> 366
 <212> PRT
 <213> Buchnera aphidicola

<400> 113
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Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Thr Asn
 35 40 45
 Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile
 50 55 60
 Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg
 65 70 75 80
 Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys
 85 90 95
 Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser
 100 105 110
 Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe
 115 120 125
 Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe
 130 135 140
 Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160
 Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg
 165 170 175
 Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser
 180 185 190
 Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn
 195 200 205
 Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg
 210 215 220
 Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu
 225 230 235 240
 Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Glu Lys Lys Asn Pro Ile
 245 250 255
 Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile
 260 265 270
 Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly
 275 280 285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
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 Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
 305 310 315 320
 Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
 325 330 335
 Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
 340 345 350
 Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
 355 360 365

<210> 114
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 114
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<210> 115
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 115
 gtgtggatcc gtggtgacct tagccac 27

<210> 116
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 116

ttcgtgtccg aggaccttgt ggtccacaac

30

<210> 117

<211> 3514

<212> DNA

<213> Aquifex aeolicus

<400> 117

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ggtacgccc caccggttctt atggcacttc aaatgaaaaa gaccattcac gaactgagtt 720
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gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcgggtg 2280
```

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```

<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

```

Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
  1             5             10             15

```

```

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
      20             25             30

```

```

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
      35             40             45

```

```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
      50             55             60

```

```

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
      65             70             75             80

```

```

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
      85             90             95

```

```

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

```

100	105	110
Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp		
115	120	125
Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
130	135	140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
165	170	175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
180	185	190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
195	200	205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
210	215	220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	235
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
245	250	255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
260	265	270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
275	280	285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
290	295	300
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
325	330	335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
340	345	350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355	360	365
Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu 370	375	380
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly 385	390	395 400
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp 405	410	415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr 420	425	430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr 435	440	445
Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met 450	455	460
Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln 465	470	475 480
Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr 485	490	495
Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile 500	505	510
Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu 515	520	525
Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg 530	535	540
His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu 545	550	555 560
Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr 565	570	575
Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp 580	585	590
Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu 595	600	605
Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu		

610		615		620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly				
625		630		635 640
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu				
	645		650	655
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg				
	660		665	670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys				
	675		680	685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val				
	690		695	700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys				
705		710		715 720
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu				
	725		730	735
Arg Lys Ala Ile Gly Lys Lys Lys Ala Asp Leu Met Ala Gln Met Lys				
	740		745	750
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys				
	755		760	765
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe				
	770		775	780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala				
785		790		795 800
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr				
	805		810	815
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys				
	820		825	830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val				
	835		840	845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg				
	850		855	860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg				

865		870		875		880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr						
	885			890		895
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala						
	900			905		910
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys						
	915			920		925
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe						
	930			935		940
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu						
945		950		955		960
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr						
	965			970		975
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu						
	980			985		990
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu						
	995			1000		1005
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu						
1010		1015		1020		
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr						
1025		1030		1035		1040
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys						
	1045			1050		1055
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val						
	1060			1065		1070
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr						
	1075			1080		1085
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu						
1090		1095		1100		
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn						
1105		1110		1115		1120
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu						

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
 1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
 1155 1160

<210> 119

<211> 2408

<212> DNA

<213> Aquifex aeolicus

<400> 119

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```

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

```

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```

```

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
      20              25              30

```

```

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
      35              40              45

```

```

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50              55              60

```

```

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
      65              70              75              80

```

```

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
      85              90              95

```

```

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
      100             105             110

```

```

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
      115             120             125

```

```

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
      130             135             140

```

```

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
      145             150             155             160

```

```

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
      165             170             175

```


Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
 180 185 190
 Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
 195 200 205
 Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
 210 215 220
 Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
 225 230 235 240
 Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
 245 250 255
 Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
 260 265 270
 Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
 275 280 285
 Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
 290 295 300
 Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
 305 310 315 320
 Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
 325 330 335
 Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
 340 345 350
 Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
 355 360 365
 Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
 370 375 380
 Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
 385 390 395 400
 Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
 405 410 415
 Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
 420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
465 470

<210> 121
<211> 1090
<212> DNA
<213> Aquifex aeolicus

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aacttaatcg taagggcaac ggacttggaa aactaccttg tagtctccgt aaagggggag 180
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aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
gtagaaggag gagaacact ttcgggaaac cttctcgta acggaataga aaaggtagag 420
tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480
gaggacagaa ttcaactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
taaacattga aaagagtga gacgagtctt ttgcttactt ctccactccc gagtggaaac 600
tcgccggttag ctccctggaag gagaattccc ggactacatg agtgtcatcc ctgaggagtt 660
ttcggcggaa gtcttggttg agacagagga agtcttaaaag gttttaaaaga ggttgaaggc 720
tttaagcgaa ggaaaagttt ttcccgtgaa gattacctta agcgaaaacc ttgccatctt 780
tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840
agagcccttt gagataggat tcaacggaaa taccttatgg aggcgcttga cgcctacgac 900
agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
gattacgaaa aggaacctta caagtgcata ataatgccga tgaggggtgta gccatgaaaa 1020
aagctttaat ctttttattg agcttgagcc ttttaattcc tgcgttttagc gaagccaaac 1080
ccaagtcttc 1090

<210> 122
<211> 363
<212> PRT
<213> Aquifex aeolicus

<400> 122
Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

20					25					30						
Phe	Leu	Leu	Ser	Ala	Lys	Glu	Glu	Asn	Leu	Ile	Val	Arg	Ala	Thr	Asp	
35					40					45						
Leu	Glu	Asn	Tyr	Leu	Val	Val	Ser	Val	Lys	Gly	Glu	Val	Glu	Glu	Glu	
50					55					60						
Gly	Glu	Val	Cys	Val	His	Ser	Gln	Lys	Leu	Tyr	Asp	Ile	Val	Lys	Asn	
65					70					75					80	
Leu	Asn	Ser	Ala	Tyr	Val	Tyr	Leu	His	Thr	Glu	Gly	Glu	Lys	Leu	Val	
85					90					95						
Ile	Thr	Gly	Gly	Lys	Ser	Thr	Tyr	Lys	Leu	Pro	Thr	Ala	Pro	Ala	Glu	
100					105					110						
Asp	Phe	Pro	Glu	Phe	Pro	Glu	Ile	Val	Glu	Gly	Gly	Glu	Thr	Leu	Ser	
115					120					125						
Gly	Asn	Leu	Leu	Val	Asn	Gly	Ile	Glu	Lys	Val	Glu	Tyr	Ala	Ile	Ala	
130					135					140						
Lys	Glu	Glu	Ala	Asn	Ile	Ala	Leu	Gln	Gly	Met	Tyr	Leu	Arg	Gly	Tyr	
145					150					155					160	
Glu	Asp	Arg	Ile	His	Phe	Val	Gly	Ser	Asp	Gly	His	Arg	Leu	Ala	Leu	
165					170					175						
Tyr	Glu	Pro	Leu	Gly	Glu	Phe	Ser	Lys	Glu	Leu	Leu	Ile	Pro	Arg	Lys	
180					185					190						
Ser	Leu	Lys	Val	Leu	Lys	Lys	Leu	Ile	Thr	Gly	Ile	Glu	Asp	Val	Asn	
195					200					205						
Ile	Glu	Lys	Ser	Glu	Asp	Glu	Ser	Phe	Ala	Tyr	Phe	Ser	Thr	Pro	Glu	
210					215					220						
Trp	Lys	Leu	Ala	Val	Arg	Leu	Leu	Glu	Gly	Glu	Phe	Pro	Asp	Tyr	Met	
225					230					235					240	
Ser	Val	Ile	Pro	Glu	Glu	Phe	Ser	Ala	Glu	Val	Leu	Phe	Glu	Thr	Glu	
245					250					255						
Glu	Val	Leu	Lys	Val	Leu	Lys	Arg	Leu	Lys	Ala	Leu	Ser	Glu	Gly	Lys	
260					265					270						
Val	Phe	Pro	Val	Lys	Ile	Thr	Leu	Ser	Glu	Asn	Leu	Ala	Ile	Phe	Glu	

275	280	285
Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu		
290	295	300
Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met		
305	310	315
		320
Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr		
	325	330
		335
Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu		
	340	345
		350
Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val		
355	360	

<210> 123
 <211> 1093
 <212> DNA
 <213> Aquifex aeolicus

<400> 123

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gaaaagtacg	gggagaatta	cacggttctg	tgggggggatg	agataagcga	ggaggaattc	180
tacactgccc	tttccgagac	cagtatattc	ggcggttcaa	aggaaaaagc	ggtggtcatt	240
tacaacttcg	gggattttct	gaagaagctc	ggaaggaaga	aaaaggaaaa	agaaaggctt	300
ataaaagtcc	tcagaaacgt	aaagagtaac	tacgtattta	tagtgtacga	tgcgaaactc	360
cagaaacagg	aactttcttc	ggaacctctg	aaatccgtag	cgtctttcgg	cggatatagt	420
gtagcaaaca	ggctgagcaa	ggagaggata	aaacagctcg	tccttaagaa	gttcaaagaa	480
aaagggataa	acgtagaaaa	cgatgccctt	gaataccttc	tccagctcac	gggttacaac	540
ttgatggagc	tcaaacttga	ggttgaaaaa	ctgatagatt	acgcaagtga	aaagaaaatt	600
ttaacactcg	atgaggtaaa	gagagtagcc	ttctcagtct	cagaaaacgt	aaacgtattt	660
gagttcgttg	atttactcct	cttaaaagat	tacgaaaagg	ctcttaaagt	tttggactcc	720
ctcatttcct	tcggaataca	ccccctccag	attatgaaaa	tcctgtcctc	ctatgctcta	780
aaactttaca	ccctcaagag	gcttgaagag	aagggagagg	acctgaataa	ggcgatggaa	840
agcgtgggaa	taaagaacaa	ctttctcaag	atgaagttca	aatcttactt	aaaggcaaac	900
tctaaagagg	acttgaagaa	cctaatactc	tccctccaga	ggatagacgc	tttttctaaa	960
ctttactttc	aggacacagt	gcagttgctg	gggattttct	gacctcaaga	ctggagaggg	1020
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ttttcccggt	tct					1093

<210> 124
 <211> 350
 <212> PRT

<213> Aquifex aeolicus

<400> 124

Val	Glu	Thr	Thr	Ile	Phe	Gln	Phe	Gln	Lys	Thr	Phe	Phe	Thr	Lys	Pro
1				5					10					15	
Pro	Lys	Glu	Arg	Val	Phe	Val	Leu	His	Gly	Glu	Glu	Gln	Tyr	Leu	Ile
			20					25					30		
Arg	Thr	Phe	Leu	Ser	Lys	Leu	Lys	Glu	Lys	Tyr	Gly	Glu	Asn	Tyr	Thr
		35					40					45			
Val	Leu	Trp	Gly	Asp	Glu	Ile	Ser	Glu	Glu	Glu	Phe	Tyr	Thr	Ala	Leu
	50					55					60				
Ser	Glu	Thr	Ser	Ile	Phe	Gly	Gly	Ser	Lys	Glu	Lys	Ala	Val	Val	Ile
65					70					75					80
Tyr	Asn	Phe	Gly	Asp	Phe	Leu	Lys	Lys	Leu	Gly	Arg	Lys	Lys	Lys	Glu
				85					90						95
Lys	Glu	Arg	Leu	Ile	Lys	Val	Leu	Arg	Asn	Val	Lys	Ser	Asn	Tyr	Val
		100						105					110		
Phe	Ile	Val	Tyr	Asp	Ala	Lys	Leu	Gln	Lys	Gln	Glu	Leu	Ser	Ser	Glu
		115					120					125			
Pro	Leu	Lys	Ser	Val	Ala	Ser	Phe	Gly	Gly	Ile	Val	Val	Ala	Asn	Arg
	130					135					140				
Leu	Ser	Lys	Glu	Arg	Ile	Lys	Gln	Leu	Val	Leu	Lys	Lys	Phe	Lys	Glu
145					150					155					160
Lys	Gly	Ile	Asn	Val	Glu	Asn	Asp	Ala	Leu	Glu	Tyr	Leu	Leu	Gln	Leu
			165					170						175	
Thr	Gly	Tyr	Asn	Leu	Met	Glu	Leu	Lys	Leu	Glu	Val	Glu	Lys	Leu	Ile
			180					185					190		
Asp	Tyr	Ala	Ser	Glu	Lys	Lys	Ile	Leu	Thr	Leu	Asp	Glu	Val	Lys	Arg
		195					200					205			
Val	Ala	Phe	Ser	Val	Ser	Glu	Asn	Val	Asn	Val	Phe	Glu	Phe	Val	Asp
	210					215					220				
Leu	Leu	Leu	Leu	Lys	Asp	Tyr	Glu	Lys	Ala	Leu	Lys	Val	Leu	Asp	Ser
225					230					235					240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
 245 250 255
 Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
 260 265 270
 Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
 275 280 285
 Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
 290 295 300
 Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
 305 310 315 320
 Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
 325 330 335
 Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
 340 345 350

<210> 125
 <211> 1051
 <212> DNA
 <213> Aquifex aeolicus

<400> 125
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 ttttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggtatt 120
 ttatgtaagg aaaacgtacc tggggatgcg gaagtgtgcc ctctgcaaa cacgtaaacg 180
 agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
 cggtaaaaag cacttcggtt accttatggg cgaacatccc gactttgtgg taataatccc 300
 gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
 gcccgcacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
 ggcggcaaac gctcttttaa aggtattgga agagccacct gcggacacca cttttatctt 480
 gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgga 540
 gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
 gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatact 660
 aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
 attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
 atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
 actctttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
 cgttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
 atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020
 ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126
 <211> 305
 <212> PRT
 <213> Aquifex aeolicus

<400> 126
 Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro
 1 5 10 15

 Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr
 20 25 30

 Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp
 35 40 45

 Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu
 50 55 60

 Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys
 65 70 75 80

 Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe
 85 90 95

 Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg
 100 105 110

 Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys
 115 120 125

 Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn
 130 135 140

 Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile
 145 150 155 160

 Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg
 165 170 175

 Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu
 180 185 190

 Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu
 195 200 205

 Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val
 210 215 220

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
 225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
 245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
 260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
 275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
 290 295 300

Asp
 305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

<400> 127
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 gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcgggt 180
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgac 240
 gagataaagg cggcggagat acatggaata accaggaag acgttgaaaa gtacggaaaag 300
 gaaccaaagg aagtaataata cgactttctg aagtaacataa agggaagcgt tctcgttggc 360
 tactacgtga agtttgacgt ctactcgtt gagaagtact ccataaagta cttccagtat 420
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
 aggagtcttg acgaccttat gaaggaactc ggtgtagaaa taagggcaag gcacaacgcc 540
 cttgaagatg cctacataac cgctcttctt ttcctaaagt acgtttaccc gaacagggag 600
 tacagactaa aggatctccc gattttcctt 630

<210> 128
 <211> 210
 <212> PRT
 <213> Aquifex aeolicus

<400> 128
 Met Asn Phe Leu Lys Lys Phe Leu Leu Arg Lys Ala Gln Lys Ser
 1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20	25	30
Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp		
35	40	45
Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn		
50	55	60
Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp		
65	70	75
Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu		
85	90	95
Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr		
100	105	110
Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser		
115	120	125
Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn		
130	135	140
Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly		
145	150	155
Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala		
165	170	175
Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu		
180	185	190
Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile		
195	200	205
Phe Leu		
210		

<210> 129
 <211> 526
 <212> DNA
 <213> Aquifex aeolicus

<400> 129
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 ccgagcgga cgcgcgtagt agagtttact ctggcttaca acagaaggta taaaaaccag 120
 aacggtgaat ttcaggagga aagtcacttc ttgacgtaa aggcgtacgg aaaaatggct 180

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gaagactggg ctacacgctt ctcgaaagga tacctcgtac tcgtagaggg aagactctcc 240
caggaaaagt gggagaaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaaggtgct gaacttcaag cagaagaaga ggaggaagtt 360
ctccccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccttt ttaattttga ggaggttaaa gtatggtagt gagagctcct 480
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

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<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

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Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
  1             5             10             15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
      20             25             30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
      35             40             45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
      50             55             60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
      65             70             75             80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
      85             90             95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
      100            105            110

Gln Ala Glu Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
      115            120            125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
      130            135            140

Ile Pro Phe
145

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<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

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atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatagacg agcacaagct acttttcagg gttcttacia acctctgggtc cgagtacggc 180
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
gaagtctgca aatatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagcccag 420
agcaggatat tttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgccgcaag acccggtatg gggaaaaccg cctttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccc tcagctgtat tttccttgga aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tatcgaatga agatttaaag aagcttgaag caagcgcaat agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaaagc tcagaaaagga aaaggaagtt gagttcgtgg cgggtggacta cttgcaactt 960
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgca gctctcccgt 1080
gaggtggaaa agaggagtga taaaagacc cagcttgagg acctcagaga atccggacag 1140
atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatccccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattg tgaagctcgc atttattaag gagtacacta agtttgcaaa cctagaagcc 1320
cttcctgaac aacctcctga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472
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<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

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Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
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Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
      20              25              30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
      35              40              45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
      50              55              60
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Phe	Val	Leu	Ile	Lys	Asp	His	Leu	Glu	Lys	Lys	Asn	Leu	Leu	Gln	Lys	
65					70					75					80	
Ile	Pro	Ile	Asp	Trp	Leu	Glu	Glu	Leu	Tyr	Glu	Glu	Ala	Val	Ser	Pro	
			85						90					95		
Asp	Thr	Leu	Glu	Glu	Val	Cys	Lys	Ile	Val	Lys	Gln	Arg	Ser	Ala	Gln	
		100						105					110			
Arg	Ala	Ile	Ile	Gln	Leu	Gly	Ile	Thr	Ser	Thr	Gln	Phe	Tyr	His	Val	
		115					120					125				
Lys	Asp	Val	Ala	Glu	Glu	Val	Ile	Glu	Leu	Ile	Tyr	Lys	Phe	Lys	Ser	
	130						135				140					
Ser	Asp	Arg	Leu	Val	Thr	Gly	Leu	Pro	Ser	Gly	Phe	Thr	Glu	Leu	Asp	
145					150					155					160	
Leu	Lys	Thr	Thr	Gly	Phe	His	Pro	Gly	Asp	Leu	Ile	Ile	Leu	Ala	Ala	
				165					170						175	
Arg	Pro	Gly	Met	Gly	Lys	Thr	Ala	Phe	Met	Leu	Ser	Ile	Ile	Tyr	Asn	
			180					185					190			
Leu	Ala	Lys	Asp	Glu	Gly	Lys	Pro	Ser	Ala	Val	Phe	Ser	Leu	Glu	Met	
		195					200					205				
Ser	Lys	Glu	Gln	Leu	Val	Met	Arg	Leu	Leu	Ser	Met	Met	Ser	Glu	Val	
	210					215					220					
Pro	Leu	Phe	Lys	Ile	Arg	Ser	Gly	Ser	Ile	Ser	Asn	Glu	Asp	Leu	Lys	
225					230					235					240	
Lys	Leu	Glu	Ala	Ser	Ala	Ile	Glu	Leu	Ala	Lys	Tyr	Asp	Ile	Tyr	Leu	
			245						250					255		
Asp	Asp	Thr	Pro	Ala	Leu	Thr	Thr	Thr	Asp	Leu	Arg	Ile	Arg	Ala	Arg	
			260					265					270			
Lys	Leu	Arg	Lys	Glu	Lys	Glu	Val	Glu	Phe	Val	Ala	Val	Asp	Tyr	Leu	
		275					280					285				
Gln	Leu	Leu	Arg	Pro	Pro	Val	Arg	Lys	Ser	Ser	Arg	Gln	Glu	Glu	Val	
	290					295					300					
Ala	Glu	Val	Ser	Arg	Asn	Leu	Lys	Ala	Leu	Ala	Lys	Glu	Leu	His	Ile	
305					310					315					320	

Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
 325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
 340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
 355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
 370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
 385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
 405 410 415

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Phe Glu Asp Ile Asp Phe
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 <212> DNA
 <213> Aquifex aeolicus

<400> 133
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<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

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Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
          35             40             45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
          50             55             60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
          65             70             75             80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
          85             90             95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
          100            105            110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
          115            120            125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
          130            135            140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
          145            150            155            160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

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Asp	Pro	Arg	Gly	Arg	Val	Ile	Gly	Phe	Gly	Gly	Arg	Arg	Ile	Val	Glu				
		195					200					205							
Asp	Lys	Ser	Pro	Lys	Tyr	Ile	Asn	Ser	Pro	Asp	Ser	Arg	Val	Phe	Lys				
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Lys	Gly	Glu	Asn	Leu	Phe	Gly	Leu	Tyr	Glu	Ala	Lys	Glu	Tyr	Ile	Lys				
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Glu	Glu	Gly	Phe	Ala	Ile	Leu	Val	Glu	Gly	Tyr	Phe	Asp	Leu	Leu	Arg				
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Leu	Phe	Ser	Glu	Gly	Ile	Arg	Asn	Val	Val	Ala	Pro	Leu	Gly	Thr	Ala				
		260					265					270							
Leu	Thr	Gln	Asn	Gln	Ala	Asn	Leu	Leu	Ser	Lys	Phe	Thr	Lys	Lys	Val				
	275						280					285							
Tyr	Ile	Leu	Tyr	Asp	Gly	Asp	Asp	Ala	Gly	Arg	Lys	Ala	Met	Lys	Ser				
	290					295					300								
Ala	Ile	Pro	Leu	Leu	Leu	Ser	Ala	Gly	Val	Glu	Val	Tyr	Pro	Val	Tyr				
305					310				315					320					
Leu	Pro	Glu	Gly	Tyr	Asp	Pro	Asp	Glu	Phe	Ile	Lys	Glu	Phe	Gly	Lys				
			325					330					335						
Glu	Glu	Leu	Arg	Arg	Leu	Ile	Asn	Ser	Ser	Gly	Glu	Leu	Phe	Glu	Thr				
		340					345					350							
Leu	Ile	Lys	Thr	Ala	Arg	Glu	Asn	Leu	Glu	Glu	Lys	Thr	Arg	Glu	Phe				
	355						360					365							
Arg	Tyr	Tyr	Leu	Gly	Phe	Ile	Ser	Asp	Gly	Val	Arg	Arg	Phe	Ala	Leu				
	370					375					380								
Ala	Ser	Glu	Phe	His	Thr	Lys	Tyr	Lys	Val	Pro	Met	Glu	Ile	Leu	Leu				
385					390				395					400					
Met	Lys	Ile	Glu	Lys	Asn	Ser	Gln	Glu	Lys	Glu	Ile	Lys	Leu	Ser	Phe				
			405				410					415							
Lys	Glu	Lys	Ile	Phe	Leu	Lys	Gly	Leu	Ile	Glu	Leu	Lys	Pro	Lys	Ile				

420

425

430

Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
 435 440 445

Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
 450 455 460

Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
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Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
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Asn Thr

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 <212> DNA
 <213> Aquifex aeolicus

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 <212> PRT
 <213> Aquifex aeolicus

<400> 136
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Asn	Leu	Asp	Thr	Tyr	His	Pro	Lys	Asn	Val	Ser	Gln	Asn	Arg	Ala	Leu	
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Leu	Thr	Ile	Arg	Val	Phe	Val	His	Asn	Phe	Asn	Pro	Glu	Glu	Gly	Lys	
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Gly	Leu	Thr	Phe	Val	Gly	Ser	Pro	Gly	Val	Gly	Lys	Thr	His	Leu	Ala	
85					90					95						
Val	Ala	Thr	Leu	Lys	Ala	Ile	Tyr	Glu	Lys	Lys	Gly	Ile	Arg	Gly	Tyr	
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Phe	Phe	Asp	Thr	Lys	Asp	Leu	Ile	Phe	Arg	Leu	Lys	His	Leu	Met	Asp	
115					120					125						
Glu	Gly	Lys	Asp	Thr	Lys	Phe	Leu	Lys	Thr	Val	Leu	Asn	Ser	Pro	Val	
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<210> 137

<211> 4101

<212> DNA

<213> *Thermatoga maritima*

<400> 137

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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
      20             25            30

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Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
      35             40            45

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Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
      50             55            60

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```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
      65             70            75            80

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Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
      85             90            95

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Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln

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	130						135					140							
Arg	Glu	Glu	Pro	Lys	Gly	Glu	Glu	Leu	Lys	Ile	Glu	Asp	Glu	Asn	His				
145					150					155					160				
Ile	Phe	Gly	Gln	Lys	Pro	Arg	Lys	Ile	Val	Phe	Thr	Pro	Ser	Lys	Ile				
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Phe	Glu	Tyr	Asn	Lys	Lys	Thr	Ser	Val	Lys	Gly	Lys	Ile	Phe	Lys	Ile				
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Glu	Lys	Ile	Glu	Gly	Lys	Arg	Thr	Val	Leu	Leu	Ile	Tyr	Leu	Thr	Asp				
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Leu	Thr	Asp	His	Gly	Asn	Val	Gln	Ala	Ile	Pro	Tyr	Phe	Tyr	Asp	Ala				
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Ala	Lys	Glu	Ala	Gly	Ile	Lys	Pro	Ile	Phe	Gly	Ile	Glu	Ala	Tyr	Leu				
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Val	Ser	Asp	Val	Glu	Pro	Val	Ile	Arg	Asn	Leu	Ser	Asp	Asp	Ser	Thr				
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355	360	365
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln 370	375	380
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg 385	390	395 400
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met 405	410	415
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly 420	425	430
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr 435	440	445
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu 450	455	460
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu 465	470	475 480
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro 485	490	495
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val 500	505	510
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu 515	520	525
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys 530	535	540
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn 545	550	555 560
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val 565	570	575
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu 580	585	590
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Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn 740 745 750		
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile 755 760 765		
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu 770 775 780		
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala 785 790 795 800		
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser 805 810 815		
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr 820 825 830		
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr 835 840 845		
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro 850 855 860		
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His		

865		870		875		880
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro						
	885			890		895
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg						
	900			905		910
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr						
	915			920		925
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr						
	930			935		940
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu						
	945			950		955
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly						
				965		970
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro						
	980			985		990
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His						
	995			1000		1005
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu						
	1010			1015		1020
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly						
	1025			1030		1035
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile						
				1045		1050
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser						
	1060			1065		1070
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg						
	1075			1080		1085
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg						
	1090			1095		1100
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg						
	1105			1110		1115
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys						

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195 1200
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275 1280
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
1345	1350	1355 1360
Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139
 <211> 567
 <212> DNA
 <213> *Thermatoga maritima*

<400> 139
 gtgctcgcca tgatatggaa cgacaccgtt ttttgcgtcg tagacacaga aaccacggga 60
 accgatccct ttgccggaga ccggatagtt gaaatagccg ctgttcctgt cttcaagggg 120
 aagatctaca gaaacaaagc gtttcactct ctcgtgaatc ccagaataag aatccctgcg 180
 ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaagcgcc agacatggac 240
 acagtttacg atcttttcag ggattacgtg aagggaacgg tgctcgtgtt tcacaacgcc 300
 aacttcgacc tcaacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
 aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcatttctctc 420
 aaatggctct ccgaaagact tgggaataaaa accacgatac ggcaccgtgc tcttccagat 480
 gccctggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttggtga aaacaggggtc 540
 aacgaattca tacgtggaaa acggggg 567

<210> 140
 <211> 189
 <212> PRT
 <213> *Thermatoga maritima*

<400> 140
 Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
 1 5 10 15
 Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
 20 25 30
 Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
 35 40 45
 His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
 50 55 60
 Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
 65 70 75 80
 Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
 85 90 95
 Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
 100 105 110
 Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
 115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
 130 135 140
 Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
 145 150 155 160
 Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
 165 170 175
 Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
 180 185

<210> 141
 <211> 1434
 <212> DNA
 <213> *Thermatoga maritima*

<400> 141
 gtggaagttc tttacaggaa gtacaggcca aagacttttt ctgaggttgt caatcaggat 60
 catgtgaaga aggcaataat cgggtgctatt cagaagaaca gcgtggccca cggatacata 120
 ttcgccggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180
 aactgtgaga acagaaaggg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
 gacgagggaa ccttcatgga cgtgatagag ctcgacgcgg cctccaacag aggaatagac 300
 gagatcagaa gaatcagaga cgccgttgga tacaggccga tggaaggtaa atacaaagtc 360
 tacataatag acgaagttca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420
 ctccaagaac ctccctccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaagggtt 480
 cctccacaga ttatctcgag atgtcagggtt ttcgagttca gaaacattcc cgacgagctc 540
 atcgaaaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaagct 600
 ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660
 caggtgtgga agttctcgga aggaaagata gatctcgaga cggtagacag ggcgctcggg 720
 ttgataccga tacagggttgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780
 agggctcttca ccgttctcga cgacgtctat tacagcggga aggactacga ggtgctcatt 840
 caggaagcag tcgaggatct ggtcgaagac ctggaaaggg agagaggggt ttaccagggtt 900
 tcagcgaacg atatagttca ggtttcgaga caacttctga atcttctgag agagataaag 960
 ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020
 tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080
 cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140
 ttcgagaaac gcttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200
 tttgtcgctc tcagcctctc agaggtgcag tttgacggag aaaaggtgat tatttctttt 1260
 gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaac 1320
 attttttcta gaaaactcgg gaaaaaagta gaagttgaac ttcgactgat gggaaaagaa 1380
 gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434

<210> 142
 <211> 478
 <212> PRT

<213> *Thermatoga maritima*

<400> 142

Met	Glu	Val	Leu	Tyr	Arg	Lys	Tyr	Arg	Pro	Lys	Thr	Phe	Ser	Glu	Val
1				5					10					15	
Val	Asn	Gln	Asp	His	Val	Lys	Lys	Ala	Ile	Ile	Gly	Ala	Ile	Gln	Lys
			20					25						30	
Asn	Ser	Val	Ala	His	Gly	Tyr	Ile	Phe	Ala	Gly	Pro	Arg	Gly	Thr	Gly
		35					40					45			
Lys	Thr	Thr	Leu	Ala	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Asn	Cys	Glu	Asn
	50					55					60				
Arg	Lys	Gly	Val	Glu	Pro	Cys	Asn	Ser	Cys	Arg	Ala	Cys	Arg	Glu	Ile
65					70					75					80
Asp	Glu	Gly	Thr	Phe	Met	Asp	Val	Ile	Glu	Leu	Asp	Ala	Ala	Ser	Asn
				85					90						95
Arg	Gly	Ile	Asp	Glu	Ile	Arg	Arg	Ile	Arg	Asp	Ala	Val	Gly	Tyr	Arg
		100						105					110		
Pro	Met	Glu	Gly	Lys	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	His	Met
		115					120					125			
Leu	Thr	Lys	Glu	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro
	130					135					140				
Pro	Ser	His	Val	Val	Phe	Val	Leu	Ala	Thr	Thr	Asn	Leu	Glu	Lys	Val
145					150					155					160
Pro	Pro	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Val	Phe	Glu	Phe	Arg	Asn	Ile
			165					170						175	
Pro	Asp	Glu	Leu	Ile	Glu	Lys	Arg	Leu	Gln	Glu	Val	Ala	Glu	Ala	Glu
		180						185					190		
Gly	Ile	Glu	Ile	Asp	Arg	Glu	Ala	Leu	Ser	Phe	Ile	Ala	Lys	Arg	Ala
	195						200					205			
Ser	Gly	Gly	Leu	Arg	Asp	Ala	Leu	Thr	Met	Leu	Glu	Gln	Val	Trp	Lys
	210					215					220				
Phe	Ser	Glu	Gly	Lys	Ile	Asp	Leu	Glu	Thr	Val	His	Arg	Ala	Leu	Gly
225					230					235					240

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
 245 250 255

Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
 260 265 270

Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
 275 280 285

Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
 290 295 300

Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
 305 310 315 320

Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
 325 330 335

Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
 340 345 350

Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
 355 360 365

Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
 370 375 380

Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
 385 390 395 400

Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
 405 410 415

Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
 420 425 430

Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
 435 440 445

Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
 450 455 460

Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
 465 470 475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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atgaaagtaa ccgtcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aattttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatggtcaag 240
gttctccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat gggtgaaaag 420
gtcatcttcg ccgctgcaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggtttctc tgtcgacaaa tgatgtagaa acggtgatga gagtggtcga cgctgaattt 720
cccgattaca aaaggggat ccccgaaact ttcaaaacga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gaggggatg gtgattgcca gcaaggggaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaaccgc 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccata gactggca 1098
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<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

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Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1              5              10             15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
      20              25             30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
      35              40             45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
      50              55             60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
      65              70             75             80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
      85              90             95
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Val	Ile	Ser	Ser	Gly	Ser	Thr	Val	Phe	Arg	Ile	Thr	Thr	Met	Pro	Ala			
				100					105					110				
Asp	Glu	Phe	Pro	Glu	Ile	Thr	Pro	Ala	Glu	Ser	Gly	Ile	Thr	Phe	Glu			
		115						120				125						
Val	Asp	Thr	Ser	Leu	Leu	Glu	Glu	Met	Val	Glu	Lys	Val	Ile	Phe	Ala			
	130						135				140							
Ala	Ala	Lys	Asp	Glu	Phe	Met	Arg	Asn	Leu	Asn	Gly	Val	Phe	Trp	Glu			
145					150					155					160			
Leu	His	Lys	Asn	Leu	Leu	Arg	Leu	Val	Ala	Ser	Asp	Gly	Phe	Arg	Leu			
				165					170					175				
Ala	Leu	Ala	Glu	Glu	Gln	Ile	Glu	Asn	Glu	Glu	Glu	Ala	Ser	Phe	Leu			
			180					185					190					
Leu	Ser	Leu	Lys	Ser	Met	Lys	Glu	Val	Gln	Asn	Val	Leu	Asp	Asn	Thr			
	195						200					205						
Thr	Glu	Pro	Thr	Ile	Thr	Val	Arg	Tyr	Asp	Gly	Arg	Arg	Val	Ser	Leu			
	210					215					220							
Ser	Thr	Asn	Asp	Val	Glu	Thr	Val	Met	Arg	Val	Val	Asp	Ala	Glu	Phe			
225					230				235					240				
Pro	Asp	Tyr	Lys	Arg	Val	Ile	Pro	Glu	Thr	Phe	Lys	Thr	Lys	Val	Val			
			245					250						255				
Val	Ser	Arg	Lys	Glu	Leu	Arg	Glu	Ser	Leu	Lys	Arg	Val	Met	Val	Ile			
			260				265						270					
Ala	Ser	Lys	Gly	Ser	Glu	Ser	Val	Lys	Phe	Glu	Ile	Glu	Glu	Asn	Val			
		275					280					285						
Met	Arg	Leu	Val	Ser	Lys	Ser	Pro	Asp	Tyr	Gly	Glu	Val	Val	Asp	Glu			
	290					295					300							
Val	Glu	Val	Gln	Lys	Glu	Gly	Glu	Asp	Leu	Val	Ile	Ala	Phe	Asn	Pro			
305				310					315					320				
Lys	Phe	Ile	Glu	Asp	Val	Leu	Lys	His	Ile	Glu	Thr	Glu	Glu	Ile	Glu			
			325					330						335				
Met	Asn	Phe	Val	Asp	Ser	Thr	Ser	Pro	Cys	Gln	Ile	Asn	Pro	Leu	Asp			
		340						345					350					

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
 355 360 365

<210> 145
 <211> 972
 <212> DNA
 <213> *Thermatoga maritima*

<400> 145
 atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
 ctctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
 gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
 atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240
 aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacaggtgg aaagggagta 300
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
 ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaagggt 420
 ggaacgaacg acctgatcat agaaaggag attgaaaaac tgaaagctta ttccgaggac 480
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
 gatgatTTTT gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
 gatctcttca aaatcctcgt tcttgtagaca aagaaaagat actacacctg gcctgatgtg 720
 tccaggggtg ccaaagagct gggaattccc gttcctcgtg tggctcgttt cctcggtttc 780
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
 gtagaaaaga tactgaggga tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
 caaaaccgt tcttcacga gtccatagaa gaggtggcac tggatgtata ttctcttcag 960
 agagatgaag aa 972

<210> 146
 <211> 324
 <212> PRT
 <213> *Thermatoga maritima*

<400> 146
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
 1 5 10 15
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
 20 25 30
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
 35 40 45
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
 50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys	65	70	75	80
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly	85	90	95	
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys	100	105	110	
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile	115	120	125	
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp	130	135	140	
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp	145	150	155	160
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln	165	170	175	
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg	180	185	190	
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser	195	200	205	
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys	210	215	220	
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val	225	230	235	240
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg	245	250	255	
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His	260	265	270	
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu	275	280	285	
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe	290	295	300	
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln	305	310	315	320

Arg Asp Glu Glu

<210> 147

<211> 936

<212> DNA

<213> *Thermatoga maritima*

<400> 147

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gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcgttc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cggaaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaaggtcct ttcaaaaggc ctcgaagggt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattctttg cgctttttga tcaggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcagggtga agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936
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<210> 148

<211> 311

<212> PRT

<213> *Thermatoga maritima*

<400> 148

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Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
  1             5             10             15

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
      20             25             30

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
      35             40             45

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
      50             55             60

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
      65             70             75             80
```

Leu	Asn	Tyr	Ser	Pro	Glu	Leu	Tyr	Thr	Arg	Lys	Tyr	Val	Ile	Val	His
				85					90					95	
Asp	Cys	Glu	Arg	Met	Thr	Gln	Gln	Ala	Ala	Asn	Ala	Phe	Leu	Lys	Ala
				100				105					110		
Leu	Glu	Glu	Pro	Pro	Glu	Tyr	Ala	Val	Ile	Val	Leu	Asn	Thr	Arg	Arg
				115				120				125			
Trp	His	Tyr	Leu	Leu	Pro	Thr	Ile	Lys	Ser	Arg	Val	Phe	Arg	Val	Val
				130			135				140				
Val	Asn	Val	Pro	Lys	Glu	Phe	Arg	Asp	Leu	Val	Lys	Glu	Lys	Ile	Gly
145					150					155					160
Asp	Leu	Trp	Glu	Glu	Leu	Pro	Leu	Leu	Glu	Arg	Asp	Phe	Lys	Thr	Ala
				165					170					175	
Leu	Glu	Ala	Tyr	Lys	Leu	Gly	Ala	Glu	Lys	Leu	Ser	Gly	Leu	Met	Glu
				180				185					190		
Ser	Leu	Lys	Val	Leu	Glu	Thr	Glu	Lys	Leu	Leu	Lys	Lys	Val	Leu	Ser
				195			200					205			
Lys	Gly	Leu	Glu	Gly	Tyr	Leu	Ala	Cys	Arg	Glu	Leu	Leu	Glu	Arg	Phe
				210			215				220				
Ser	Lys	Val	Glu	Ser	Lys	Glu	Phe	Phe	Ala	Leu	Phe	Asp	Gln	Val	Thr
225					230					235					240
Asn	Thr	Ile	Thr	Gly	Lys	Asp	Ala	Phe	Leu	Leu	Ile	Gln	Arg	Leu	Thr
				245					250					255	
Arg	Ile	Ile	Leu	His	Glu	Asn	Thr	Trp	Glu	Ser	Val	Glu	Asp	Lys	Ser
				260				265					270		
Val	Ser	Phe	Leu	Asp	Ser	Ile	Leu	Arg	Val	Lys	Ile	Ala	Asn	Leu	Asn
				275				280				285			
Asn	Lys	Leu	Thr	Leu	Met	Asn	Ile	Leu	Ala	Ile	His	Arg	Glu	Arg	Lys
				290			295				300				
Arg	Gly	Val	Asn	Ala	Trp	Ser									
305					310										

<210> 149

<211> 423
 <212> DNA
 <213> *Thermatoga maritima*

<400> 149
 atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
 tacacgctca gcggaactcc agtcaccacc ttcaccatag cggtggacag gggtcccaga 120
 aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctttgaaga 180
 ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaagggtgaa 240
 atgagaatga gaagatggga aacacccact ggagaaaaga gggatatctcc ggaggttggtc 300
 gcaaacggtg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
 gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
 ttt 423

<210> 150
 <211> 141
 <212> PRT
 <213> *Thermatoga maritima*

<400> 150
 Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
 1 5 10 15
 Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
 20 25 30
 Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
 35 40 45
 Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
 50 55 60
 Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
 65 70 75 80
 Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
 85 90 95
 Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
 100 105 110
 Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
 115 120 125
 Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
 130 135 140

<210> 151
 <211> 1353
 <212> DNA
 <213> *Thermatoga maritima*

<400> 151
 atgCGTgttc ccccgCacaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
 gatccgctcg taataaacga cgttcttgaa attttgagcc acgaagattt ctatctgaaa 120
 aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
 gtgggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240
 ctggaagtgg ccagctcgc tgaggctgtg ccagttctg cacacgcact tctactacgcg 300
 gagatcgta aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
 gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420
 ttcgagatct cagagatgaa aacgacaaaa tcctacgata atctgagagg catcatgcac 480
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga acccgggtgtg 540
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac aggggtccac 600
 agctccgata tgggtgataat agcagcgaga ccctccatgg gaaaaacctc ctctgcactc 660
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
 atgtccaagg aacagctcgc tcaaagacta ctacgcatgg agtccggtgt ggatctttac 780
 agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggtctct 840
 aaactctaca aagcaccat agttgtggac gatgagtcac tcctcgatcc gcgacgttg 900
 agggcaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tctcgactat 960
 ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
 tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tgggtgatagc gctttcacag 1080
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
 tccggtgcga tagaacagga cgcagacaca gtcatttca tctacaggga ggaatattac 1200
 aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260
 ataggtaaac agagaaacgg tcccgttgga acgatcactc tgatcttoga cccagaacg 1320
 gttacgttcc atgaagtcga tgtggtgcat tca 1353

<210> 152
 <211> 451
 <212> PRT
 <213> *Thermatoga maritima*

<400> 152
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
 1 5 10 15
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
 20 25 30
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
 35 40 45
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50		55		60
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp				
65		70		75 80
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala				
	85		90	95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu				
	100		105	110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp				
	115		120	125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser				
	130		135	140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His				
145		150		155 160
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile				
	165		170	175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu				
	180		185	190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala				
	195		200	205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg				
	210		215	220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu				
225		230		235 240
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly				
	245		250	255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp				
	260		265	270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val				
	275		280	285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala				
	290		295	300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr				

305 310 315 320
 Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu
 325 330 335
 Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp
 340 345 350
 Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg
 355 360 365
 Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile
 370 375 380
 Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr
 385 390 395 400
 Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu
 405 410 415
 Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile
 420 425 430
 Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val
 435 440 445
 Val His Ser
 450

<210> 153
 <211> 1695
 <212> DNA
 <213> *Thermatoga maritima*

<400> 153
 gtgattcctc gagaggtcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60
 tccgagtacg tgaatcttac ccgggtaggt tctcctaca gggctctctg tccctttcat 120
 tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
 tgcggtgcga gtggagacgt catcaaattt cttcaagaaa tggaagggat cagtttccag 240
 gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300
 gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360
 aaagagctgg agaaatcgaa agaggcaaaa gactatttaa aaagcagagg cttctctgaa 420
 gaagatatag caaagttcgg ctttgggtac gtccccaaga gatccagcat ctctatagaa 480
 gttgcagaag gcatgaacat aacactggaa gaacttgtca gatacggtat cgcgctgaaa 540
 aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600
 agtggtcata ttgtggcttt tgggtggcgt gctctcggca acgaagaacc gaagtatttg 660
 aactctccag agaccaggta tttttcgaag aagaagacct tttttctctt cgatgaggcg 720

```

aaaaaagtgg caaaagaggt tggttttttc gtcatcacccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgtattcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaattcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgtgg caacccccctc tccttacaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaaac tcgcgttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc cccgcgggtg tgagatccta ctttctttc 1140
ctcaaaggtt gggtcacaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaaggt ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg
1695

```

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
  1             5             10             15

```

```

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
      20             25             30

```

```

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
      35             40             45

```

```

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
      50             55             60

```

```

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
      65             70             75             80

```

```

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
      85             90             95

```

```

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
      100            105            110

```

```

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
      115            120            125

```

Ala	Lys	Asp	Tyr	Leu	Lys	Ser	Arg	Gly	Phe	Ser	Glu	Glu	Asp	Ile	Ala	
130						135					140					
Lys	Phe	Gly	Phe	Gly	Tyr	Val	Pro	Lys	Arg	Ser	Ser	Ile	Ser	Ile	Glu	
145					150					155					160	
Val	Ala	Glu	Gly	Met	Asn	Ile	Thr	Leu	Glu	Glu	Leu	Val	Arg	Tyr	Gly	
				165					170					175		
Ile	Ala	Leu	Lys	Lys	Gly	Asp	Arg	Phe	Val	Asp	Arg	Phe	Glu	Gly	Arg	
			180					185					190			
Ile	Val	Val	Pro	Ile	Lys	Asn	Asp	Ser	Gly	His	Ile	Val	Ala	Phe	Gly	
		195					200					205				
Gly	Arg	Ala	Leu	Gly	Asn	Glu	Glu	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	
	210					215					220					
Thr	Arg	Tyr	Phe	Ser	Lys	Lys	Lys	Thr	Leu	Phe	Leu	Phe	Asp	Glu	Ala	
225					230					235					240	
Lys	Lys	Val	Ala	Lys	Glu	Val	Gly	Phe	Phe	Val	Ile	Thr	Glu	Gly	Tyr	
				245					250					255		
Phe	Asp	Ala	Leu	Ala	Phe	Arg	Lys	Asp	Gly	Ile	Pro	Thr	Ala	Val	Ala	
		260						265					270			
Val	Leu	Gly	Ala	Ser	Leu	Ser	Arg	Glu	Ala	Ile	Leu	Lys	Leu	Ser	Ala	
		275					280					285				
Tyr	Ser	Lys	Asn	Val	Ile	Leu	Cys	Phe	Asp	Asn	Asp	Lys	Ala	Gly	Phe	
	290					295					300					
Arg	Ala	Thr	Leu	Lys	Ser	Leu	Glu	Asp	Leu	Leu	Asp	Tyr	Glu	Phe	Asn	
305					310					315					320	
Val	Leu	Val	Ala	Thr	Pro	Ser	Pro	Tyr	Lys	Asp	Pro	Asp	Glu	Leu	Phe	
				325					330					335		
Gln	Lys	Glu	Gly	Glu	Gly	Ser	Leu	Lys	Lys	Met	Leu	Lys	Asn	Ser	Arg	
			340					345					350			
Ser	Phe	Glu	Tyr	Phe	Leu	Val	Thr	Ala	Gly	Glu	Val	Phe	Phe	Asp	Arg	
		355					360					365				
Asn	Ser	Pro	Ala	Gly	Val	Arg	Ser	Tyr	Leu	Ser	Phe	Leu	Lys	Gly	Trp	
	370					375					380					

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400
 Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415
 Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430
 Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445
 Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460
 Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480
 Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495
 Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510
 Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525
 Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540
 Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560
 Lys Ile Lys Arg Arg
 565

<210> 155
 <211> 804
 <212> DNA
 <213> *Thermus thermophilus*

<400> 155
 atggctctac acccggtctca ccctggggca ataatcgggc acgaggccgt tctcgccctc 60
 ctccccgcc tcaccgccca gaccctgctc ttctccggcc ccgagggggt ggggaggcgc 120
 accgtggccc gctggtacgc ctgggggctc aaccgcggct tcccccgcc ctccctgggg 180
 gagcaccgg acgtcctcga ggtggggccc aaggcccgg acctccggg ccgggcccag 240

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gtgcggctgg aggaggtggc gccctcttg gagtgggtgt ccagccaccc ccgggagcgg 300
gtgaaggtgg ccatcctgga ctcggccac ctctcaccg aggcgcgcgc caacgccctc 360
ctcaagctcc tggaggagcc ccttctctac gcccgcatcg tcctcatcgc cccaagccgc 420
gccaccctcc tccccaccct ggctctccgg gccacggagg tggcattcgc ccccggtgcc 480
gaggaggccc tgcgcgccct caccaggac ccggagctcc tccgctacgc cgccggggcc 540
ccgggcccgc tccttagggc cctccaggac ccggaggggt accggggccc catggccagg 600
gcgcaaaggg tcctgaaagc cccgccctg gagcgcctcg ctttgcttcg ggagcttttg 660
gccgaggagg aggggggtcca cgccctccac gccgtcctaa agcgcccgga gcacctcctt 720
gccctggagc gggcgcgga ggccctggag ggggtacgtga gccccgagct ggtcctcgcc 780
cggctggcct tagacttaga gaca 804

```

<210> 156

<211> 268

<212> PRT

<213> *Thermus thermophilus*

<400> 156

```

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
  1              5              10              15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
      20              25              30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
      35              40              45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
      50              55              60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
      65              70              75              80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
      85              90              95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
      100             105             110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
      115             120             125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
      130             135             140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
      145             150             155             160

```

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
 165 170 175

 Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
 180 185 190

 Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
 195 200 205

 Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
 210 215 220

 Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
 225 230 235 240

 Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
 245 250 255

 Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
 260 265

<210> 157
 <211> 729
 <212> DNA
 <213> *Thermus thermophilus*

<400> 157
 atgctggacc tgagggaggt gggggaggcg gaggtggaagg ccctaaagcc ccttttggaa 60
 agcgtgcccc agggcgcccc cgtcctcctc ctggacccta agccaagccc ctcccgggcg 120
 gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
 cggcacctgg aaaaccgggc caagcgccctg gggctcaggc tcccgggcgg ggtggcccag 240
 tacctggcct ccctggaggg ggacctcgag gccctggagc gggagctgga gaagcttgcc 300
 ctccctctccc caccctcac cctggagaag gtggagaagg tggaggccct gaggcccccc 360
 ctacagggct ttgacctggt gcgctccgtc ctggagaagg accccaagga ggccctcctg 420
 cgcctaggcg gcctcaagga ggagggggag gagccctca ggctcctcgg ggccctctcc 480
 tggcagttcg cctcctcgc ccgggccttc ttctcctcc gggaaaacc caggcccaag 540
 gaggaggacc tcgcccgcct cgaggccac ccctacgccg ccgcccgcgc cctggaggcg 600
 gcgaagcgcc tcacggaaga ggccctcaag gaggccttg acgcccctcat ggaggcgga 660
 aagagggcca agggggggaa agaccctggt ctgccttg aggcggcggt cctccgcctc 720
 gcccgttga 729

<210> 158
 <211> 292
 <212> PRT
 <213> *Thermus thermophilus*

<400> 158

Met	Val	Ile	Ala	Phe	Thr	Gly	Asp	Pro	Phe	Leu	Ala	Arg	Glu	Ala	Leu
1				5					10					15	
Leu	Glu	Glu	Ala	Arg	Leu	Arg	Gly	Leu	Ser	Arg	Phe	Thr	Glu	Pro	Thr
			20					25					30		
Pro	Glu	Ala	Leu	Ala	Gln	Ala	Leu	Ala	Pro	Gly	Leu	Phe	Gly	Gly	Gly
		35					40					45			
Gly	Ala	Met	Leu	Asp	Leu	Arg	Glu	Val	Gly	Glu	Ala	Glu	Trp	Lys	Ala
	50					55					60				
Leu	Lys	Pro	Leu	Leu	Glu	Ser	Val	Pro	Glu	Gly	Val	Pro	Val	Leu	Leu
65					70					75				80	
Leu	Asp	Pro	Lys	Pro	Ser	Pro	Ser	Arg	Ala	Ala	Phe	Tyr	Arg	Asn	Arg
			85						90					95	
Glu	Arg	Arg	Asp	Phe	Pro	Thr	Pro	Lys	Gly	Lys	Asp	Leu	Val	Arg	His
			100					105					110		
Leu	Glu	Asn	Arg	Ala	Lys	Arg	Leu	Gly	Leu	Arg	Leu	Pro	Gly	Gly	Val
		115					120					125			
Ala	Gln	Tyr	Leu	Ala	Ser	Leu	Glu	Gly	Asp	Leu	Glu	Ala	Leu	Glu	Arg
	130					135					140				
Glu	Leu	Glu	Lys	Leu	Ala	Leu	Leu	Ser	Pro	Pro	Leu	Thr	Leu	Glu	Lys
145				150					155					160	
Val	Glu	Lys	Val	Val	Ala	Leu	Arg	Pro	Pro	Leu	Thr	Gly	Phe	Asp	Leu
			165					170					175		
Val	Arg	Ser	Val	Leu	Glu	Lys	Asp	Pro	Lys	Glu	Ala	Leu	Leu	Arg	Leu
		180						185					190		
Gly	Gly	Leu	Lys	Glu	Glu	Gly	Glu	Glu	Pro	Leu	Arg	Leu	Leu	Gly	Ala
		195					200					205			
Leu	Ser	Trp	Gln	Phe	Ala	Leu	Leu	Ala	Arg	Ala	Phe	Phe	Leu	Leu	Arg
	210					215					220				
Glu	Asn	Pro	Arg	Pro	Lys	Glu	Glu	Asp	Leu	Ala	Arg	Leu	Glu	Ala	His
225					230					235				240	
Pro	Tyr	Ala	Ala	Arg	Arg	Ala	Leu	Glu	Ala	Ala	Lys	Arg	Leu	Thr	Glu
			245					250					255		

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gtgtgtcata tgagtaagga tttcgtccac cttcacc 37

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat ccgggggacta ctcggaagta aggg 34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaaccac aatattccag ttccag 36

<210> 162

<211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 162
 gtgtgtggat ccttatccac catgagaagt atttttcac 39

 <210> 163
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 163
 gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41

 <210> 164
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 164
 gtgtgtggat ccttaatccg cctgaacggc taacg 35

 <210> 165
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 165
 gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

 <210> 166

<211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 166
 gtgtgtggat ccttaaaaca gcctcgtccc gctgga 36

 <210> 167
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 167
 gtgtgtcata tgcgcgttaa ggtggacagg gag 33

 <210> 168
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 168
 tgtgtctcga gtcattggcta caccctcatc ggcatt 35

 <210> 169
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 169
 gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg 47

 <210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct cttcatcg 39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171
atggctcgag gcctgaaccg cgttttcctc atcggcgccc tcgccaccg gccggacatg 60
cgctacaccc cggcgggggt cgccattttg gacctgacct tcgccggtca ggacctgctt 120
ctttccgata acggggggga accggaggtg tcctggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcttgaggt accgccagt ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggacccccctg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360
agcccagget ccgcgcgcc ctgaaccagg tcttcctcat gggcaacctg acccgggacc 420
cggaactccg ctacaccccc cagggcaccg cggtgggccc gctgggcctg gcggtgaacg 480
agcgccgcca gggggcggag ggcgcaccc acttcgtgga ggttcaggcc tggcgcgacc 540
tggcggagtg ggccgcccag ctgaggaagg gcgacggcct ttctgtgatc ggcaggttg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccgt gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccgg 780
aggaggatth gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
 50 55 60
 Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly
 65 70 75 80
 Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu
 85 90 95
 Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys
 100 105 110
 Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu
 115 120 125
 Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg
 130 135 140
 Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn
 145 150 155 160
 Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln
 165 170 175
 Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp
 180 185 190
 Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser
 195 200 205
 Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu
 210 215 220
 Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg
 225 230 235 240
 Ser Arg Glu Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu
 245 250 255
 Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe
 260 265

<210> 173

<211> 992

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 173

```
aattccgaca tttcaattga atcgtttatt cgcgttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgtagct caggcgcgct ttttctctga aatcgtgaaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccc acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaata cgggctgatt tattgaaaac cgtgattcgg 300
caaacgggtg tcgccgtttc tacatcgga acgcgcccaa tcttgacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcacgctt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cggaggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggtt gcttgacggc 600
aactatccgg agacggccc cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttgtga aactgacgac gcttcctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgcgggc gcttgatgga acagacattt 900
caaatcagct tctactggggc catgcggccg ttctgttgc gcccgcttca accgattcga 960
tgcttcagct cattttgccg gtgagaacat at 992
```

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
  1                      5                      10                      15
```

```
Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
                20                      25                      30
```

```
Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
                35                      40                      45
```

```
Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
                50                      55                      60
```

```
Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
                65                      70                      75                      80
```

```
Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
                85                      90                      95
```

```
Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
                100                     105                     110
```

```
Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
```

115	120	125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys		
130	135	140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly		
145	150	155 160
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His		
165	170	175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu		
180	185	190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr		
195	200	205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala		
210	215	220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu		
225	230	235 240
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu		
245	250	255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu		
260	265	270
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala		
275	280	285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln		
290	295	300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His		
305	310	315 320
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr		
325	330	

<210> 175

<211> 492

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 175

```

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cacgtttacg ctcgcggtca accgtccgtt taaaaatcag 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcgttt ggcgccgcca ggcggaaaac 180
gtcgccaact ttttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaaccgcg 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcatcg atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt                                     492

```

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

```

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

```

```

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
          20             25             30

```

```

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
          35             40             45

```

```

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
          50             55             60

```

```

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
          65             70             75             80

```

```

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
          85             90             95

```

```

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
          100            105            110

```

```

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
          115            120            125

```

```

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
          130            135            140

```

```

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
          145            150            155            160

```

```

Asp Leu Pro Phe

```

<210> 177
 <211> 1044
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 177
 atgctggaac gcgtatgggg aaacattgaa aaacggcggtt tttctcccct ttatttatta 60
 tacggcaatg agccgttttt attaacggaa acgtatgagc gattggtgaa cgcagcgctt 120
 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
 gcggcgcttg aggaggccga gacggtgccg ttttcggcg agcggcggtgt cattctcatc 240
 aagcatccat attttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgccgtac 360
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
 caaggggagc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
 ctttcgcctt tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
 atcgaggcgg cggcggttga gcggcctgtc gccgcacgc cggaagaaaa cgtattttgtg 660
 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
 cttgaaaaca atgaagagcc gatcaaaatt ttggcggttg tcgccgcca tttccgcttg 780
 ctttcgcaag tgaaatggct tgcctcetta ggctacggac aggcgcaaat tgctgcggcg 840
 ctcaaggtgc acccggttccg cgtcaagctc gctcttgctc aagcggcccc cttcgctgac 900
 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960
 gcggtcgacg gccgggttggc cgttgagctg cttctgatgc gctggggcgc ccgcccggcg 1020
 caagcggggc gccacggccg gcgg 1044

<210> 178
 <211> 348
 <212> PRT
 <213> *Bacillus stearothermophilus*

<400> 178
 Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
 1 5 10 15
 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65		70		75		80
Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His						
	85			90		95
Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser						
	100			105		110
Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys						
	115			120		125
Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro						
	130			135		140
Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser						
	145			150		155
Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg						
		165		170		175
Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala						
		180		185		190
Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg						
	195			200		205
Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln						
	210			215		220
Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu						
	225			230		235
Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala						
		245		250		255
His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr						
	260			265		270
Gly Gln Ala Gln Ile Ala Ala Ala Leu Lys Val His Pro Phe Arg Val						
	275			280		285
Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala						
	290			295		300
Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly						
	305			310		315
Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Leu Met Arg Trp Gly						

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
 340 345

<210> 179
 <211> 757
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 179
 atgcgatggg aacagctagc gaaacgccag ccggtggtgg cgaaaatgct gcaaagcggc 60
 ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
 aaagcggcca gtttggttgtt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
 ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
 gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
 ttctcgaaaa cagcggtcga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
 atgacgacaa gcgctgccaa cagccttctg aaattttttg aagagccgca tccggggacg 420
 gtggcggtat tgctgactga gcaataccac cgcctgctag ggacgatcgt ttcccgtgt 480
 caagtgtttt cgttccggcc gttgccgccc gcagagctcg cccagggact tgtcgaggag 540
 cacgtgccgt tgccgttggc gctgttggct gccatttga caaacagctt cgaggaagca 600
 ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
 gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
 catttttttg aaagccatca gcttgacctt ggacttg 757

<210> 180
 <211> 252
 <212> PRT
 <213> *Bacillus stearothermophilus*

<400> 180
 Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
 1 5 10 15
 Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
 20 25 30
 Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
 35 40 45
 Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
 50 55 60
 Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
 65 70 75 80

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
 85 90 95
 Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
 100 105 110
 Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
 115 120 125
 Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
 130 135 140
 Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
 145 150 155 160
 Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
 165 170 175
 Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
 180 185 190
 Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
 195 200 205
 Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
 210 215 220
 Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
 225 230 235 240
 His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
 245 250

<210> 181
 <211> 1677
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 181
 gtggcatacc aagcgttata tcgctgtgtt cggccgcagc gctttgcgga catggtcggc 60
 caagaacacg tgaccaagac gttgcaaagc gccctgcttc aacataaaat atcgcacgct 120
 tacttatattt ccggccccgcg cggtagcagga aaaacgagcg cagcgaaaat ttctcgccaag 180
 gcggtcaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgccctc 240
 ggcattacga atggaacggt tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
 gtcgatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgccaacgtc ggcccgcgtac 360
 aaagtgtata tcatcgacga ggtgcatatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
 aaaacgttgg aggagccgcc gaaacacgtc attttcattt tggccacgac cgagccgcac 480


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aaaattccgg cgacgatcat ttcccgtcgc caacgggttcg attttcgccg catcccgtt 540
caggcgatcg ttccacggct aaagtacgtc gcaagcgccc aaggtgtcga ggcgtcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatttgc cgccttatcg agcttcacg aagccatcca ccgcaaagat 780
acagcggcgg ttcttcagca cttggaaacg atgatggcgc aagggaaaga tccgcatcgt 840
ttggttgaag acttgatttt gtactatcgc gatttattgc tgtacaaaac cgctccctat 900
gtggagggag cgattcaaat tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
attccggttt ccaatttata cgaggccatc gagttgctga acaaaagcca gcaagagatg 1020
aagtggacaa accaccgcgc ccttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgccg ccccgctcgt gtcggcttcc gagttggaac cgttgataaa gcggattgaa 1140
acgctggagg cggaattgcg gcgcctgaag gaacaaccgc ctgcccctcc gtcgaccgcc 1200
gcgccggtga aaaaactgtc caaaccgatg aaacggggg gatataaagc cccggttggc 1260
cgcatttacg agctgttgaa acaggcgacg catgaagatt tagcttttgt gaaaggatgc 1320
tgggcggatg tgctcgacac gttgaaacgg cagcataaag tgtcgcacgc tgccttgctg 1380
caagagagcg agccggttgc agcgagcgcc tcagcgtttg tattaataatt caaatacgaa 1440
atccactgca aaatggcgac cgatcccaca agttcgggtc aagaaaacgt cgaagcgatt 1500
ttgtttgagc tgacaaaccg ccgctttgaa atggtagcca ttccggaggg agaatgggga 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggcgaagagc tgatcgaaat taaagaa 1677

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<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

```

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
  1              5              10              15

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
          20              25              30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
          35              40              45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
          50              55              60

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
          65              70              75              80

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
          85              90              95

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
          100             105             110

```

Phe	Ala	Pro	Thr	Ser	Ala	Arg	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	115	120	125
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140
Glu	Pro	Pro	Lys	His	Val	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155
Lys	Ile	Pro	Ala	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Arg	165	170	175
Arg	Ile	Pro	Leu	Gln	Ala	Ile	Val	Ser	Arg	Leu	Lys	Tyr	Val	Ala	Ser	180	185	190
Ala	Gln	Gly	Val	Glu	Ala	Ser	Asp	Glu	Ala	Leu	Ser	Ala	Ile	Ala	Arg	195	200	205
Ala	Ala	Asp	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220
Ile	Ser	Phe	Ser	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Asp	Val	Leu	Ala	Met	225	230	235
Thr	Gly	Ala	Ala	Ser	Phe	Ala	Ala	Leu	Ser	Ser	Phe	Ile	Glu	Ala	Ile	245	250	255
His	Arg	Lys	Asp	Thr	Ala	Ala	Val	Leu	Gln	His	Leu	Glu	Thr	Met	Met	260	265	270
Ala	Gln	Gly	Lys	Asp	Pro	His	Arg	Leu	Val	Glu	Asp	Leu	Ile	Leu	Tyr	275	280	285
Tyr	Arg	Asp	Leu	Leu	Leu	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Glu	Gly	Ala	290	295	300
Ile	Gln	Ile	Ala	Val	Val	Asp	Glu	Ala	Phe	Thr	Ser	Leu	Ser	Glu	Met	305	310	315
Ile	Pro	Val	Ser	Asn	Leu	Tyr	Glu	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Ser	325	330	335
Gln	Gln	Glu	Met	Lys	Trp	Thr	Asn	His	Pro	Arg	Leu	Leu	Leu	Glu	Val	340	345	350
Ala	Leu	Val	Lys	Leu	Cys	His	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Ser	355	360	365

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380
 Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400
 Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415
 Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430
 Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445
 Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460
 Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480
 Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495
 Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510
 Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525
 Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
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<210> 183

<211> 4301

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 183

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 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatacg 240

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cagcttgacg	tcagcgtcga	gccgtccaag	caagaaatgg	aacagttttt	ggcgcaaaaa	540
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aaggccgcgt	ctgcgccgcc	gtccgggtccg	cttgatcatcg	gctatccgat	ccgcgacgag	660
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<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

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Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
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Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35             40             45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50             55             60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65             70             75             80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
      85             90             95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100            105            110

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Asp	Trp	Leu	Ser	Arg	Gln	Thr	Pro	Glu	Leu	Lys	Gly	Asn	Lys	Leu	Leu	115	120	125	
Val	Val	Ala	Arg	His	Glu	Ala	Glu	Ala	Leu	Ala	Ile	Lys	Arg	Arg	Phe	130	135	140	
Ala	Lys	Lys	Ile	Ala	Asp	Val	Tyr	Ala	Ser	Phe	Gly	Phe	Pro	Pro	Leu	145	150	155	160
Gln	Leu	Asp	Val	Ser	Val	Glu	Pro	Ser	Lys	Gln	Glu	Met	Glu	Gln	Phe	165	170	175	
Leu	Ala	Gln	Lys	Gln	Gln	Glu	Asp	Glu	Glu	Arg	Ala	Leu	Ala	Val	Leu	180	185	190	
Thr	Asp	Leu	Ala	Arg	Glu	Glu	Glu	Lys	Ala	Ala	Ser	Ala	Pro	Pro	Ser	195	200	205	
Gly	Pro	Leu	Val	Ile	Gly	Tyr	Pro	Ile	Arg	Asp	Glu	Glu	Pro	Val	Arg	210	215	220	
Arg	Leu	Glu	Thr	Ile	Val	Glu	Glu	Glu	Arg	Arg	Val	Val	Val	Gln	Gly	225	230	235	240
Tyr	Val	Phe	Asp	Ala	Glu	Val	Ser	Glu	Leu	Lys	Ser	Gly	Arg	Thr	Leu	245	250	255	
Leu	Thr	Met	Lys	Ile	Thr	Asp	Tyr	Thr	Asn	Ser	Ile	Leu	Val	Lys	Met	260	265	270	
Phe	Ser	Arg	Asp	Lys	Glu	Asp	Ala	Glu	Leu	Met	Ser	Gly	Val	Lys	Lys	275	280	285	
Gly	Met	Trp	Val	Lys	Val	Arg	Gly	Ser	Val	Gln	Asn	Asp	Thr	Phe	Val	290	295	300	
Arg	Asp	Leu	Val	Ile	Ile	Ala	Asn	Asp	Leu	Asn	Glu	Ile	Ala	Ala	Asn	305	310	315	320
Glu	Arg	Gln	Asp	Thr	Ala	Pro	Glu	Gly	Glu	Lys	Arg	Val	Glu	Leu	His	325	330	335	
Leu	His	Thr	Pro	Met	Ser	Gln	Met	Asp	Ala	Val	Thr	Ser	Val	Thr	Lys	340	345	350	
Leu	Ile	Glu	Gln	Ala	Lys	Lys	Trp	Gly	His	Pro	Ala	Ile	Ala	Val	Thr	355	360	365	

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys
 370 375 380
 Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp
 385 390 395 400
 Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu
 405 410 415
 Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
 420 425 430
 Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu
 435 440 445
 Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser
 450 455 460
 Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp
 465 470 475 480
 Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly
 485 490 495
 Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu
 500 505 510
 Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val
 515 520 525
 Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn
 530 535 540
 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 545 550 555 560
 His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met
 565 570 575
 Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu
 580 585 590
 Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro
 595 600 605
 Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
 610 615 620

Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro
625 630 635 640
Arg Ile Pro Arg Ser Val Leu Val Lys His Arg Asp Gly Leu Leu Val
645 650 655
Gly Ser Gly Cys Asp Lys Gly Glu Leu Phe Asp Asn Leu Ile Gln Lys
660 665 670
Ala Pro Glu Glu Val Glu Asp Ile Ala Arg Phe Tyr Asp Phe Leu Glu
675 680 685
Val His Pro Pro Asp Val Tyr Lys Pro Leu Ile Glu Met Asp Tyr Val
690 695 700
Lys Asp Glu Glu Met Ile Lys Asn Ile Ile Arg Ser Ile Val Ala Leu
705 710 715 720
Gly Glu Lys Leu Asp Ile Pro Val Val Ala Thr Gly Asn Val His Tyr
725 730 735
Leu Asn Pro Glu Asp Lys Ile Tyr Arg Lys Ile Leu Ile His Ser Gln
740 745 750
Gly Gly Ala Asn Pro Leu Asn Arg His Glu Leu Pro Asp Val Tyr Phe
755 760 765
Arg Thr Thr Asn Glu Met Leu Asp Cys Phe Ser Phe Leu Gly Pro Glu
770 775 780
Lys Ala Lys Glu Ile Val Val Asp Asn Thr Gln Lys Ile Ala Ser Leu
785 790 795 800
Ile Gly Asp Val Lys Pro Ile Lys Asp Glu Leu Tyr Thr Pro Arg Ile
805 810 815
Glu Gly Ala Asp Glu Glu Ile Arg Glu Met Ser Tyr Arg Arg Ala Lys
820 825 830
Glu Ile Tyr Gly Asp Pro Leu Pro Lys Leu Val Glu Glu Arg Leu Glu
835 840 845
Lys Glu Leu Lys Ser Ile Ile Gly His Gly Phe Ala Val Ile Tyr Leu
850 855 860
Ile Ser His Lys Leu Val Lys Lys Ser Leu Asp Asp Gly Tyr Leu Val
865 870 875 880

Gly	Ser	Arg	Gly	Ser	Val	Gly	Ser	Ser	Phe	Val	Ala	Thr	Met	Thr	Glu	885	890	895
Ile	Thr	Glu	Val	Asn	Pro	Leu	Pro	Pro	His	Tyr	Val	Cys	Pro	Asn	Cys	900	905	910
Lys	His	Ser	Glu	Phe	Phe	Asn	Asp	Gly	Ser	Val	Gly	Ser	Gly	Phe	Asp	915	920	925
Leu	Pro	Asp	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Thr	Lys	Tyr	Lys	Lys	Asp	930	935	940
Gly	His	Asp	Ile	Pro	Phe	Glu	Thr	Phe	Leu	Gly	Phe	Lys	Gly	Asp	Lys	945	950	955
Val	Pro	Asp	Ile	Asp	Leu	Asn	Phe	Ser	Gly	Glu	Tyr	Gln	Pro	Arg	Ala	965	970	975
His	Asn	Tyr	Thr	Lys	Val	Leu	Phe	Gly	Glu	Asp	Asn	Val	Tyr	Arg	Ala	980	985	990
Gly	Thr	Ile	Gly	Thr	Val	Ala	Asp	Lys	Thr	Ala	Tyr	Gly	Phe	Val	Lys	995	1000	1005
Ala	Tyr	Ala	Ser	Asp	His	Asn	Leu	Glu	Leu	Arg	Gly	Ala	Glu	Ile	Asp	1010	1015	1020
Leu	Ala	Ala	Gly	Cys	Thr	Gly	Val	Lys	Arg	Thr	Thr	Gly	Gln	His	Pro	1025	1030	1035
Gly	Gly	Ile	Ile	Val	Val	Pro	Asp	Tyr	Met	Glu	Ile	Tyr	Asp	Phe	Thr	1045	1050	1055
Pro	Ile	Gln	Tyr	Pro	Ala	Asp	Asp	Thr	Ser	Ser	Glu	Trp	Arg	Thr	Thr	1060	1065	1070
His	Phe	Asp	Phe	His	Ser	Ile	His	Asp	Asn	Leu	Leu	Lys	Leu	Asp	Ile	1075	1080	1085
Leu	Gly	His	Asp	Asp	Pro	Thr	Val	Ile	Arg	Met	Leu	Gln	Asp	Leu	Ser	1090	1095	1100
Gly	Ile	Asp	Pro	Lys	Thr	Ile	Pro	Thr	Asp	Asp	Pro	Asp	Val	Met	Gly	1105	1110	1115
Ile	Phe	Ser	Ser	Thr	Glu	Pro	Leu	Gly	Val	Thr	Pro	Glu	Gln	Ile	Met	1125	1130	1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
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 1155 1160 1165
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 1170 1175 1180
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 1235 1240 1245
 Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
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 1265 1270 1275 1280
 His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
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 Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
 1345 1350 1355 1360
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 1365 1370 1375
 Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
 1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
 1395 1400 1405

 Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
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 Pro Asp His Asn Gln Leu Ser Leu Phe
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 <210> 185
 <211> 199
 <212> PRT
 <213> *Thermus thermophilus*

 <400> 185
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 35 40 45

 Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
 50 55 60

 Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
 65 70 75 80

 Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
 85 90 95

 Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
 100 105 110

 Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
 115 120 125

 Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
 130 135 140

 Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
 145 150 155 160

 Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
 180 185 190

Ala Gly Gln Pro Arg Val Asp
 195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

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27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

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27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

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 cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggag 180
 gagggggagg agccccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240
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 gagggcccacc cctacgccgc caagaaggcc a 331

<210> 189

<211> 110
 <212> PRT
 <213> Thermus thermophilus

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 35 40 45
 Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
 50 55 60
 Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
 65 70 75 80
 Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
 85 90 95
 Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
 100 105 110

<210> 190
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 190
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31

<210> 191
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ccttctc

27

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 192

ctccgtcctg gagaaggacc ccaag

25

<210> 193

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> primer_bind

<222> (15)

<223> S at position 15 can be either C or G

<220>

<221> primer_bind

<222> (27)

<223> S at position 27 can be either C or G

<400> 193

cgcggaattca acgcsctcct caagacsct

29

<210> 194

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 194

gacacttaac atatgggtcat cgccttcacc g

31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196
<211> 10
<212> PRT
<213> *Deinococcus radiodurans*

<400> 196
Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197
<211> 10
<212> PRT
<213> *Methanococcus jannaschii*

<400> 197
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198
<211> 10
<212> PRT
<213> *Thermotoga maritima*

<400> 198
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 199
ctggtgaacc cgggctccgt gggccagc

28

<210> 200
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 200
Leu Leu Val Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 201
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 201
ctcgaggagc ttgaggaggg tgttggc

27

<210> 202
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 202
Ala Asn Thr Leu Leu Lys Leu Leu Glu
1 5

<210> 203
<211> 32
<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly
20 25 30

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga

30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccg cgtggagctc cac

33

<210> 210
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 210
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
1 5 10

<210> 211
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 211
ggctttccca tatggctcta caccggctc ac 32

<210> 212
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 212
gcgtggatcc acggtcatgt ctctaagtc 29